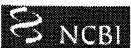
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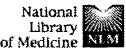
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L18	TGFb OR TGF-b OR TGFbeta OR TGF-beta	6726	L18
L17	transforming-growth-factor-beta	4	L17
L16	L15 AND beta	208	L16
L15	L12 AND TGF	220	L15
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L10	fusion-protein OR chimeric-protein	254	L10
L9	L8 AND mature	1711	L9
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Entrez-PubMed Page 1 of 10





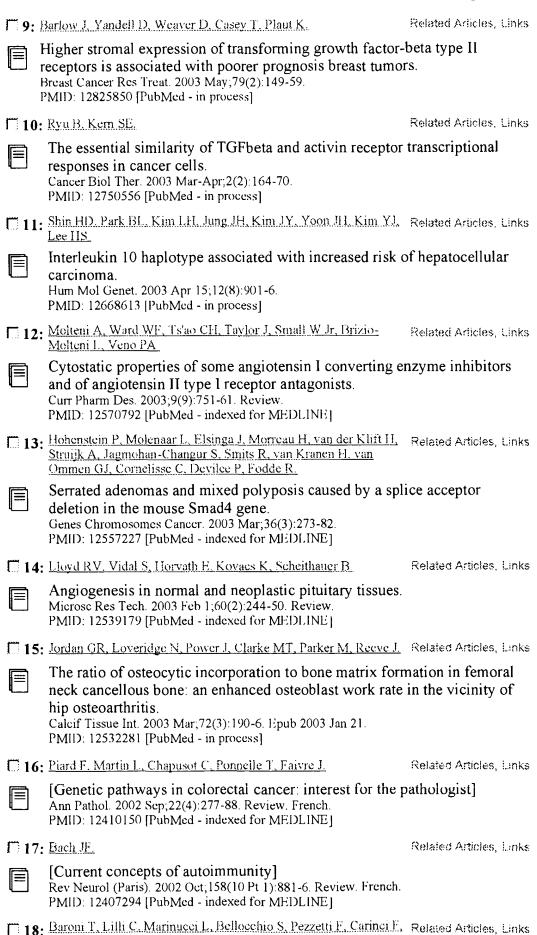


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	als.gov Central			pulmonary Am J Respir	nepatocyte grow fibrosis. Crit Care Med. 20 7024 [PubMed - as	03 Aug 28 [E <sub>j</sub>	pub ahead o		idiopathi	С	
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Association of transforming growth factor beta genes with quantitative trait loci for antibody response kinetics in hens.

Anim Genet. 2003 Aug;34(4):275-82.

PMID: 12873215 [PubMed - in process]



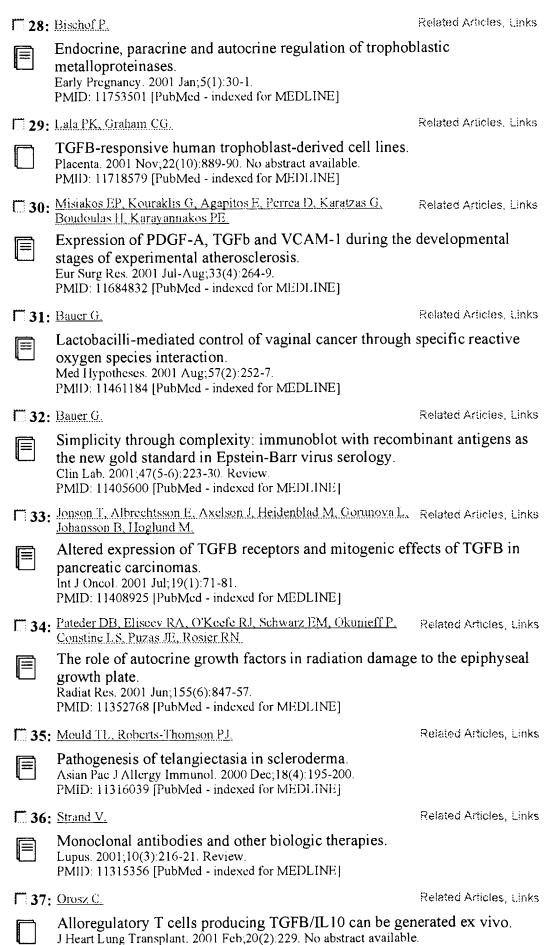
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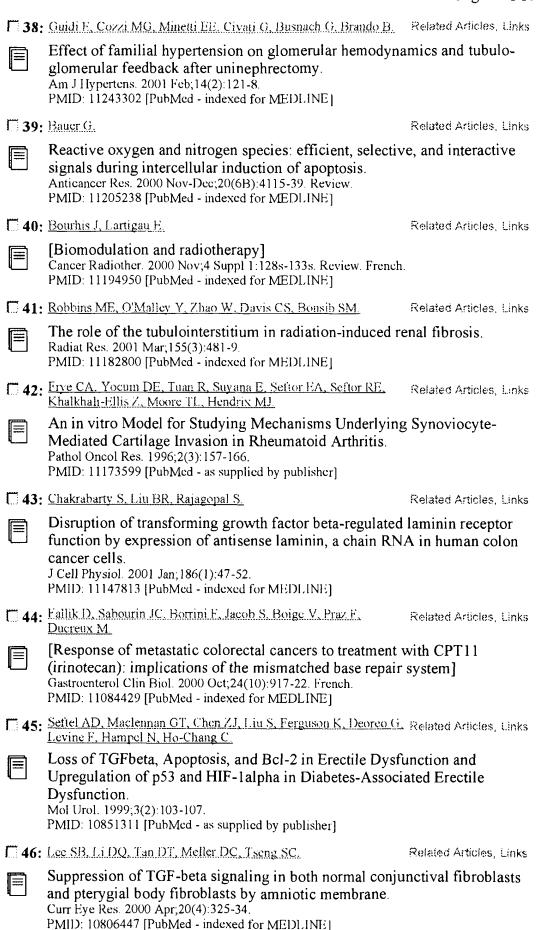
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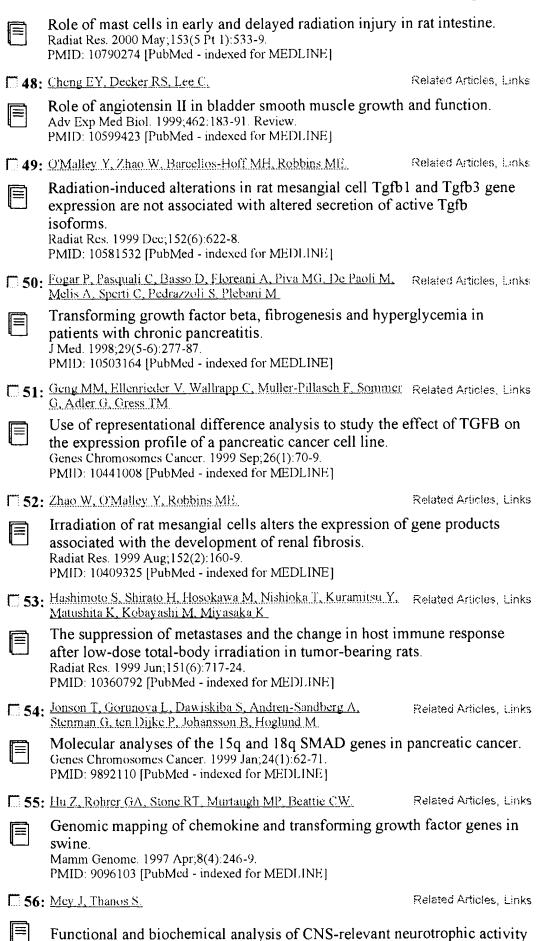


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Entrez-PubMed Page 5 of 10



Entrez-PubMed Page 6 of 10



in the lesioned sciatic nerve of adult rats.

J Hirnforsch. 1996;37(1):25-50.

Entrez-PubMed Page 7 of 10

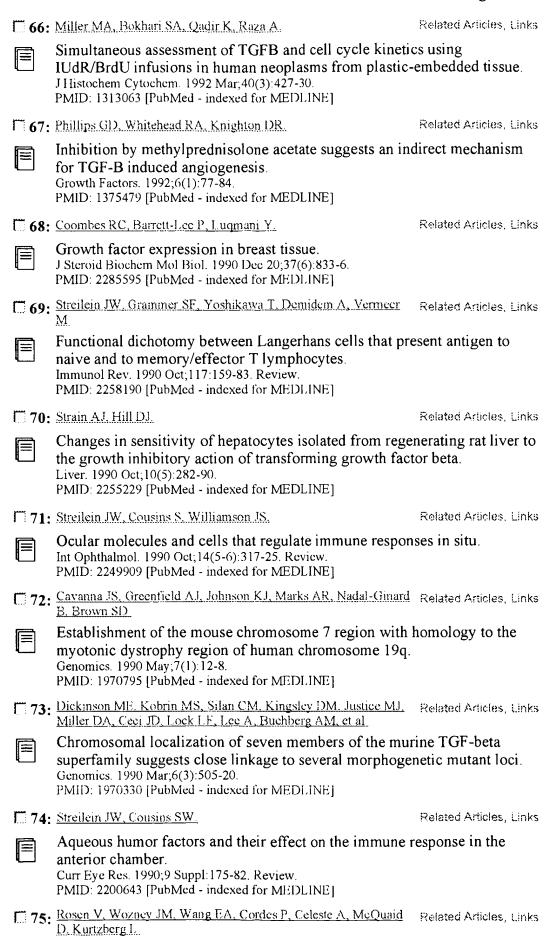
PMID: 8964975 [PubMed - indexed for MEDLINE] 57: Ace Cl. Okulicz WC. Related Articles, Links Differential gene regulation by estrogen and progesterone in the primate endometrium. Mol Cell Endocrinol. 1995 Nov 30;115(1):95-103. PMID: 8674869 [PubMed - indexed for MEDLINE] 58: Spanakis E, Brouty-Boye D. Related Articles, Links Quantitative variation of proto-oncogene and cytokine gene expression in isolated breast fibroblasts. Int J Cancer. 1995 May 29;61(5):698-705. Erratum in: Int J Cancer 1995 Nov 15;63 (4):609.PMID: 7768644 [PubMed - indexed for MEDLINE] 59. Bhattacharyya N, Ramsammy R, Eatman E, Hollis VW, Anderson Related Articles, Links <u>WA.</u> Protooncogene, growth factor, growth factor receptor, and estrogen and progesterone receptor gene expression in the immature rat uterus after treatment with estrogen and tamoxifen. J Submicrosc Cytol Pathol. 1994 Apr;26(2):147-62. PMID: 8019941 [PubMed - indexed for MEDLINE] **60:** Williams ΔC, Hague A, Manning ΔM, Van der Stappen JW, Related Articles, Links Paraskeva C In vitro models of human colorectal cancer. Cancer Surv. 1993;16:15-29. Review. PMID: 8348534 [PubMed - indexed for MEDLINE] Related Articles, Links 61: Mathews I.S. Vale WW. Molecular and functional characterization of activin receptors. Receptor. 1993 Fall;3(3):173-81. Review. PMID: 8167568 [PubMed - indexed for MEDLINE] Related Articles, Links 62: Allannie H. Guilhem I, Maugendre D. [Is thyroid hormone useful in the prevention of nodular recurrence after hemithyroidectomy?] Ann Endocrinol (Paris). 1993;54(4):286-90. Review. French. PMID: 8092805 [PubMed - indexed for MEDLINE] 63: Stampfer MR, Yaswen P. Related Articles, Links Culture systems for study of human mammary epithelial cell proliferation, differentiation and transformation. Cancer Surv. 1993;18:7-34. Review. PMID: 8013001 [PubMed - indexed for MEDLINE] [ 64: Hendricks-Taylor LR, Bachinski LL, Siciliano MJ, Fertitta Δ, Related Articles, Links Trask B, de Jong P.J. Ledbetter DH, Darlington GJ The CCAAT/enhancer binding protein (C/EBP alpha) gene (CEBPA) maps to human chromosome 19q13.1 and the related nuclear factor NF-IL6 (C/EBP beta) gene (CEBPB) maps to human chromosome 20q13.1. Genomics. 1992 Sep;14(1):12-7. PMID: 1427819 [PubMed - indexed for MEDLINE] 65: Lee SW, Tomasetto C, Paul D, Keyomarsi K, Sager R. Related Articles, Links

J Cell Biol. 1992 Sep;118(5):1213-21. PMID: 1324944 [PubMed - indexed for MEDLINE]

communication in human mammary tumor cell lines.

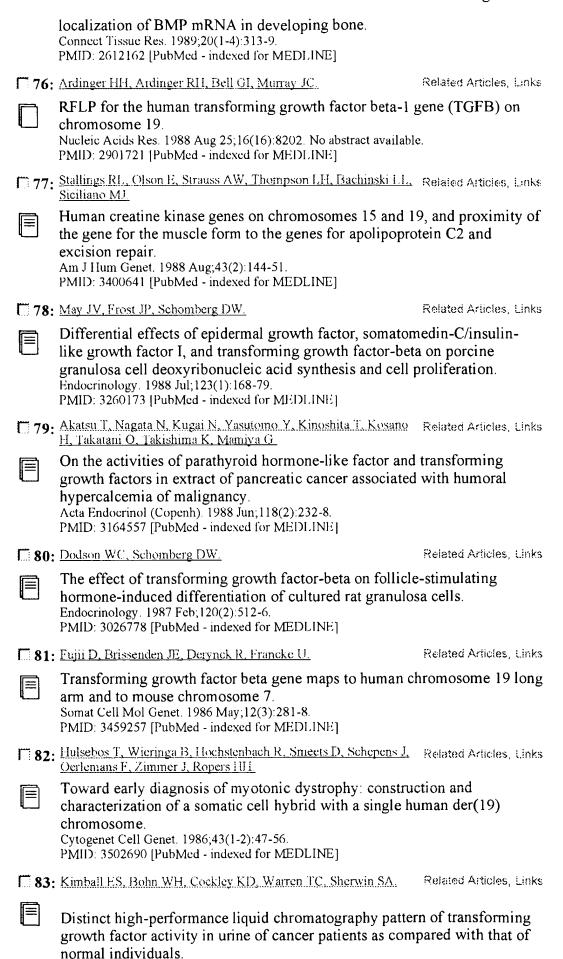
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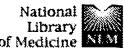
Entrez-PubMed Page 9 of 10



Cancer Res. 1984 Aug;44(8):3613-9.







of Medicine Protein Structure PMO Taxonomy MIMO Book Search PubMed • for transforming growth factor beta AND tag Go Clear Preview/Index History Clipboard Details About Entrez Show: 200 Sort Display Summary Send to Text Items 1-26 of 26 One page. Text Version 1. Cao W, Mattagajasingh SN, Xu H, Kim K, Fierlbeck W, Deng J. Related Articles, Links Lowenstein CJ, Ballermann BJ Entrez PubMed Overview TIMAP, a novel CAAX box protein regulated by TGF-beta1 and expressed Help | FAQ in endothelial cells. Tutorial Am J Physiol Cell Physiol. 2002 Jul;283(1):C327-37. New/Noteworthy PMID: 12055102 [PubMed - indexed for MEDLINE] E-Utilities 2: Lin W, Zhang N, Qin R. Related Articles, Links PubMed Services Journals Database [Effect of aldose reductase expression by transforming growth factor-beta1 MeSH Database on rat mesangial cell] Single Citation Matcher Zhonghua Yi Xue Za Zhi. 2001 Jun 25;81(12):744-7. Chinese. Batch Citation Matcher Clinical Quenes PMID: 11798960 [PubMed - indexed for MEDLINE] LinkOut 1 3: Melhuish TA, Gallo CM, Wotton D. Cubby Related Articles, Links TGIF2 interacts with histone deacetylase 1 and represses transcription. Related Resources J Biol Chem. 2001 Aug 24;276(34):32109-14. Epub 2001 Jun 26. Order Documents PMID: 11427533 [PubMed - indexed for MEDLINE] NLM Gateway TOXNET 4: Breitkopf K, Lahme B, Tag CG, Gressner AM. Related Articles, Links Consumer Health Clinical Alerts Expression and matrix deposition of latent transforming growth factor beta ClinicalTrials gov binding proteins in normal and fibrotic rat liver and transdifferentiating PubMed Central hepatic stellate cells in culture. Hepatology. 2001 Feb;33(2):387-96. Privacy Policy PMID: 11172340 [PubMed - indexed for MEDLINE] 5: Gomez-Escobar N, Gregory WF, Maizels RM. Related Articles, Links Identification of tgh-2, a filarial nematode homolog of Caenorhabditis elegans daf-7 and human transforming growth factor beta, expressed in microfilarial and adult stages of Brugia malavi. Infect Immun. 2000 Nov;68(11):6402-10. PMID: 11035752 [PubMed - indexed for MEDLINE] 6: Ji X, Chen D, Xu C, Harris SE, Mundy GR, Yoneda T. Related Articles, Links Patterns of gene expression associated with BMP-2-induced osteoblast and adipocyte differentiation of mesenchymal progenitor cell 3T3-F442A. J Bone Miner Metab. 2000;18(3):132-9. PMID: 10783846 [PubMed - indexed for MEDLINE] 7: Bassuk JA, Pichler R, Rothmier JD, Pippen J, Gordon K, Meek RL, Related Articles, Links Bradshaw AD, Lombardi D, Strandjord TP, Reed M, Sage EH, Couser WG, Johnson R

8: Maroulakou IG, Shibata MA, Anver M. Jorcyk CL, Liu M, Roche Related Articles, Links N. Roberts AB, Tsarfaty I, Reseau J, Ward J, Green JE

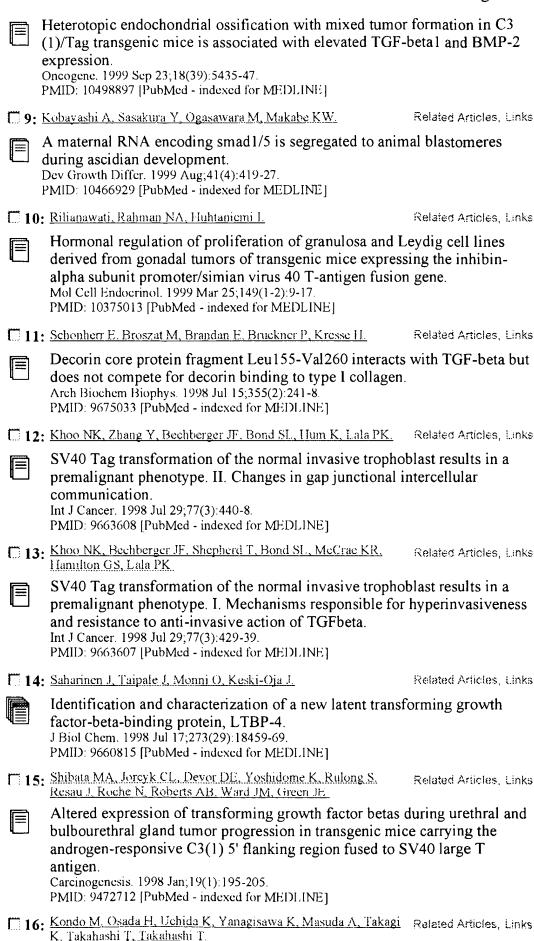
Induction of TGF-beta1 by the matricellular protein SPARC in a rat model

of glomerulonephritis.

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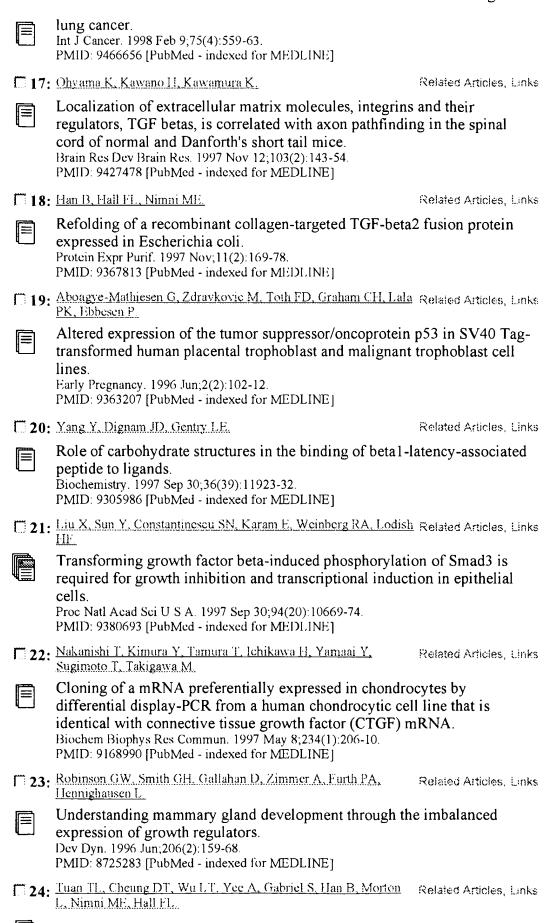
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Entrez-PubMed Page 2 of 4



Molecular cloning of human TAK1 and its mutational analysis in human

Entrez-PubMed Page 3 of 4



Engineering, expression and renaturation of targeted TGF-beta fusion

proteins.

Connect Tissue Res. 1996;34(1):1-9

Entrez-PubMed Page 4 of 4

Items 1-26 of 26

PMID: 8835843 [PubMed - indexed for MEDLINE]

25: Henis YI, Moustakas A, Lin HY, Lodish HF.

The types II and III transforming growth factor-beta receptors form homooligomers.

J Cell Biol. 1994 Jul;126(1):139-54.

PMID: 8027173 [PubMed - indexed for MEDLINE]

26: Moses III.

Related Articles, Links

TGF-beta regulation of epithelial cell proliferation.

Mol Reprod Dev. 1992 Jun;32(2):179-84. Review.

PMID: 1637556 [PubMed - indexed for MEDLINE]

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Department of Biochemistry, The Cancer Institute of the Japanese
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                 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 11 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      2002:742821 CAPLUS
AN
DN
      138:71843
      Rhesus monocyte-derived dendritic cells modified to over-express
ΤI
     TGF-.beta.1 exhibit potent veto activity
Asiedu, Clement; Dong, Sai S.; Pereboev, Alexander; Wang, Weila; Navarro,
Jesus; Curiel, David T.; Thomas, Judith M.
Division of Transplant Immunology, Department of Surgery, University of
Alabama at Birmingham, Birmingham, AL, USA
CS
      Transplantation (2002), 74(5), 629-637 CODEN: TRPLAU; ISSN: 0041-1337
50
      Lippincott Williams & Wilkins
PB
DT
      Journal
      English
LA
RE.CNT 38
                 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 12 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2002:332053 CAPLUS
AN
      136:354178
DN
TI
      Novel therapeutic vaccine formulations comprising microparticles of weak
      immunogenic antigen and chitosan
IN
      Beier, Anne Mette; Gautam, Anand; Mouritsen, Soren
PA
      Pharmexa A/S, Den.
      PCT Int. Appl., 97 pp.
SO
      CODEN: PIXXD2
DT
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LA
      English
FAN.CNT 1
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                         A2
      WO 2002034287
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                           Á5
      AU 2002010407
                                  20020506
                                                   AU 2002-10407
                                                                        20011026
PRAI DK 2000-1606
                                  20001027
     US 2000-245166P
                           Р
                                  20001103
     DK 2001-936
                           Α
                                  20010618
     WO 2001-DK705
                           W
                                  20011026
     ANSWER 13 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
      2002:218657 CAPLUS
ΑN
```

137:135411

DN

```
***factor*** -. ***beta***
                                          .1-stimulated Mv1Lu epithelial cells: Rad51
      as a target of TGF.beta.1-dependent regulation of DNA repair
ΑU
      Kanamoto, Takashi; Hellman, Ulf; Heldin, Carl-Henrik; Souchelnytskyi,
      Serhiy
CS
      Ludwig Institute for Cancer Research, Uppsala, SE-751 24, Swed.
      EMBO Journal (2002), 21(5), 1219-1230 CODEN: EMJODG; ISSN: 0261-4189
SO
      Oxford University Press
PB
      Journal
DT
      English
L.A
RE.CNT 47
                THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 14 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2001:868525 CAPLUS
ΑN
DN
      136:15216
     Methods for identifying modulators of the interaction between LAP (latency
TI
      associated peptide) and integrin .alpha.v.beta.3, and medical use thereof
IN
      Ludbrook, Steven; Barry, Simon; Horgan, Carmel; Miller, David
      Glaxo Group Limited, UK
PA
      PCT Int. Appl., 44 pp.
SO
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LA
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                                                  -----
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                               20030226
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          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
               IE, SI, LT, LV, FI, RO, MK, CY, AL, TR. 76315 A1 20030918 US 2003-
      us 2003176315
                                                 us 2003-276947
                                                                     20030505
PRAI GB 2000-12991
                                20000526
                          Α
      GB 2001-286
                          Α
                                20010105
     WO 2001-GB2352
                                20010525
                          W
                THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 11
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 15 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     2001:808437 CAPLUS
ΑN
DN
     136:96576
TI
      Connective tissue growth factor is secreted through Golgi and is degraded
      in endosome
     Chen, Youjun; Segarini, Patricia; Raoufi, Fahimeh; Bradham, Douglass; Leask, Andrew
CS
      FibroGen, Inc., South San Francisco, CA, 94080, USA
     Experimental Cell Research (2001), 271(1), 109-117
SO
     CODEN: ECREAL; ISSN: 0014-4827
PB
     Academic Press
DT
      Journal
     English
LA
RE.CNT 39
                THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L3
     ANSWER 16 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      2001:730469 CAPLUS
AN
DN
     136:84625
TI
     Biological insights into TCR.gamma..delta.+ and TCR.alpha..beta.+
      intraepithelial lymphocytes provided by serial analysis of gene expression
AU
     Shires, John; Theodoridis, Efstathios; Hayday, Adrian C.
     Peter Gorer Department of Immunobiology Guy's, King's, Medical School King's College, University of London, London, SE1 9RT, UK
CS
SO
      Immunity (2001), 15(3), 419-434
     CODEN: IUNIEH; ISSN: 1074-7613
```

PR

Cell Press

```
English
RE.CNT 64
               THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 17 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     2001:582046 CAPLUS
AN
     135:176996
DN
TI
     Use of dendroaspin as vehicle for non-dendroaspin domains and
     pharmaceutical uses of chimeric proteinss
     Lu, Xinjie; Kakkar, Vijay Vir
IN
PA
     Trigen Limited, UK
     PCT Int. Appl., 39 pp.
SO
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DT
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LA
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FAN.CNT 1
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PΙ
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              DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG. 20102 A1 20020829 US 2001-779054 20010205
     US 2002120102
                                               EP 2001-949004
     EP 1252313
                         Α2
                               20021030
                                                                  20010205
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI GB 2000-2625 A 20000205
     WO 2001-GB439
                         W
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     ANSWER 18 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
     2000:897036 CAPLUS
AΝ
     134:51915
DN
TI
     The transcriptional co-activator P/CAF potentiates TGF-.beta./smad
     signaling
     Itoh, Susumu; Ericsson, Johan; Nishikawa, Jun-Ichi; Heldin, Carl-Henrik;
     Ten Dijke, Peter
     Division of Cellular Biochemistry, The Netherlands Cancer Institute,
CS
     Amsterdam, 1066 CX, Neth.
SO
     Nucleic Acids Research (2000), 28(21), 4291-4298
     CODEN: NARHAD; ISSN: 0305-1048
PR
     Oxford University Press
DT
     Journal
     English
LA
RE.CNT
        53
               THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 19 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
     2000:856761 CAPLUS
AN
DN
     134:145499
     Regulation of a multigenic invasion program by the transcription factor,
TI
     AP-1: re-expression of a down-regulated gene, TSC-36, inhibits invasion
ΑU
     Johnston, Imogen M. P.; Spence, Heather J.; Winnie, Joseph N.; McGarry,
     Lynn; Vass, J. Keith; Meagher, Liam; Stapleton, Genevieve; Ozanne,
     Bradford W.
     CRC Beatson Laboratories, Beatson Institute for Cancer Research, Glasgow,
CS
     G61 1BD, UK
     Oncogene (2000), 19(47),
                                5348-5358
SO
     CODEN: ONCNES; ISSN: 0950-9232
     Nature Publishing Group
PR
DT
     Journal
LA
     English
               THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
        95
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 20 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
ΑN
     2000:735226 CAPLUS
```

Development of a Recombinant Bacterial Expression System for the Active

DN

TT

134:305914

```
Type II Receptor Ligand Binding Domain
ΑU
     Boesen, Christian C.; Motyka, Shawn A.; Patamawenu, Apisit; Sun, Peter D.
     Structural Biology Section, Laboratory of Immunogenetics, National
CS
     Institute of Allergy and Infectious Diseases, National Institutes of
     Health, Rockville, MD, 20852, USA
Protein Expression and Purification (2000), 20(1), 98-104
SO
     CODEN: PEXPEJ; ISSN: 1046-5928
PB
     Academic Press
DT
     Journal
     English
LA
RE.CNT 12
              THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 21 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2000:695991 CAPLUS
AN
     133:305996
DN
TI
     Role of Smad proteins and transcription factor Sp1 in p21Waf1/Cip1
                                         ***growth***
     regulation by ***transforming***
                                                            ***factor*** -.
       ***beta***
ΑU
     Pardali, Katerina; Kurisaki, Akira; Moren, Anita; ten Dijke, Peter;
     Kardassis, Dimitris; Moustakas, Aristidis
     Ludwig Institute for Cancer Research, Uppsala, SE-751 24, Swed.
CS
S0
     Journal of Biological Chemistry (2000), 275(38), 29244-29256
     CODEN: JBCHA3; ISSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
LA
RE.CNT 63
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L3
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     2000:241521 CAPLUS
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                     proteins of ***functional***
ng*** ***growth*** ***fac
       ***Fusion***
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                                               ***factor*** . ***beta***
       ***transforming***
     family of proteins and their prepn., biol. activity and uses
IN
     Oppermann, Hermann; Tai, Mei-Sheng; McCartney, John
     Stryker Corporation, USA
PA
SO
     PCT Int. Appl., 162 pp.
     CODEN: PIXXD2
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LA
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FAN.CNT 3
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     wo 2000020607
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     ANSWER 23 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2000:241494 CAPLUS
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       ***Fusion***
                      proteins of
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TI
                                                      domains of the
       family of proteins and their preparation, biological activity and uses
     Oppermann, Hermann; Tai, Mei-Sheng; McCartney, John
IN
PA
     Stryker Corporation, USA
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     PCT Int. Appl., 149 pp.
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```

```
AU, CA, JP
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     US 1999-374936
                            19990816
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     WO 1999-US23370
                            19991007
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L3
     ANSWER 24 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
AN
     2000:240985 CAPLUS
DN
     132:292701
     Novel methods for therapeutic vaccination
TI
IN
     Steinaa, Lucilla; Mouritsen, Soren; Nielsen, Klaus Gregorious; Haaning,
     Jesper; Leach, Dana; Dalum, Iben; Gautam, Anand; Birk, Peter; Karlsson,
     Gunilla
PA
     M & E Biotech A/S, Den.
     PCT Int. Appl., 220 pp.
SO
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                                           HR 2001-319
                                                             20010504
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     WO 1999-DK525
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                            19991005
L3
     ANSWER 25 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     1999:673041
                 CAPLUS
DN
     131:282025
TI
     Improved methods for making hormone heterodimers for therapeutic and
     disagnostic purposes
TN
     Moyle, William R.
PA
     University of Medicine & Dentistry of New Jersey, USA
SO
     PCT Int. Appl., 73 pp.
     CODEN: PIXXD2
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LA
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FAN.CNT 1
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                                           AU 1999-35561
                                                            19990413
PRAI US 1998-59625
                       Α
                            19980414
```

19990413

W

wo 1999-US8018

## ALL CITATIONS AVAILABLE IN THE RE FORMAT

```
L3
     ANSWER 26 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1999:672013 CAPLUS
AN
DN
      132:31626
TI
     c-Jun transactivates the promoter of the human p21WAF1/Cip1 gene by acting
     as a superactivator of the ubiquitous transcription factor Sp1
     Kardassis, Dimitris; Papakosta, Paraskevi; Pardali, Katerina; Moustakas,
ΑU
CS
     Department of Basic Sciences, University of Crete Medical School and
      Institute of Molecular Biology and Biotechnology, Foundation of Research
     and Technology of Hellas, Crete, GR-71110, Greece
50
     Journal of Biological Chemistry (1999), 274(41), 29572-29581
     CODEN: JBCHA3; IŠSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
LA
RE.CNT 71
               THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L3
     ANSWER 27 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
AN
     1999:104567 CAPLUS
     130:291720
DN
        ***Functional***
                            association of TGF-.beta. receptor II with cyclin B
TI
     Liu, Jin Hong; Wei, Sheng; Burnette, Pearlie K.; Gamero, Ana M.; Hutton, Michael; Djeu, Julie Y.
ΑU
     Immunology Program, H Lee Moffitt Cancer Center and Research Institute,
     Department of Biochemistry and Molecular Biology, University of South Florida, Tampa, FL, 33612, USA Oncogene (1999), 18(1), 269-275
SO
     CODEN: ONCNES; ISSN: 0950-9232
PB
     Stockton Press
DT
     Journal
     English
LA
RE.CNT 39
               THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 28 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     1998:805570 CAPLUS
     130:91225
DN
     SMAD3/4-dependent transcriptional activation of the human type VII
TI
     collagen gene (COL7A1) promoter by ***transforming***
***factor*** ***beta***
                                                                      ***growth***
ΑU
     Vindevoghel, Laurence; Lechleider, Robert J.; Kon, Atsushi; De Caestecker,
     Mark P.; Uitto, Jouni; Roberts, Anita B.; Mauviel, Alain
CS
     Department of Dermatology and Cutaneous Biology, Jefferson Medical
     College, Jefferson Institute of Molecular Medicine, Thomas Jefferson
     University, Philadelphia, PA, 19107, USA
Proceedings of the National Academy of Sciences of the United States of
America (1998), 95(25), 14769-14774
CODEN: PNASA6; ISSN: 0027-8424
SO
PB
     National Academy of Sciences
DT
     Journal
LA
     English
RE.CNT 39
               THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
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     1998:803928 CAPLUS
AN
DN
     130:62035
                     ***functional***
TI
     sequence and
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     for human chordin
IN
     Lavallie, Edward R.; Racie, Lisa A.; Derobertis, Edward M.
     Genetics Institute, Inc., USA
PA
S0
     U.S., 22 pp., Cont.-in-part of U.S. 5,679,783.
     CODEN: USXXAM
DT
     Patent
     English
LA
FAN.CNT 3
                       KIND DATE
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PΙ
     us 5846770
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     us 5679783
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     wo 9821335
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```

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,

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                         Α1
                                19980603
                                                  AU 1997-48960
                                19991116
      us 5986056
                          Α
                                                  US 1998-130032
                                                                      19980804
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                                 19941122
      US 1996-749169
                                 19961114
      WO 1997-US18151
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         56
                THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 30 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      1998:790670 CAPLUS
ΑN
DN
      130:34762
     Smad2 mutants and Smad-binding Smad2 peptides and methods for inhibiting ***transforming*** ***growth*** ***factor*** ***beta***
TI
      signal transduction
      Souchelnytskyi, Serhiy; Tamaki, Kiyoshi; Engstrom, Ulla; Wernstedt, Christer; Piek, Esther; Ten, Dijke Peter; Henrik, Carl
IN
P\Delta
      Ludwig Institute for Cancer Research, USA
S<sub>0</sub>
      PCT Int. Appl., 83 pp.
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DT
      Patent
LA
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PΙ
      wo 9853066
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                          Р
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                          W
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                          Α3
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RE.CNT
                THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 31 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
      1998:685114 CAPLUS
DN
      129:313128
TI
      Characterizing a cellular response to a stimulus using a lumiphore
      genetically modified with a signal pathway component
IN
      Thastrup, Ole; Petersen Bjorn, Sara; Tullin, Soren; Kasper, Almholt;
      Scudder, Kurt
PA
     Novo Nordisk A/s, Den.
SO
     PCT Int. Appl., 327 pp.
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LA
     English
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```

```
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      AT 215227
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                          A2
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      ES 2173573
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                                                 ES 1998-913541
                                                                     19980407
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                                20030211
      us 6518021
                                                                     19991007
                          В1
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                          Α1
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                                                                     20020205
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                                19970407
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      EP 1998-913541
                                19980407
                          Α3
     WO 1998-DK145
                                19980407
                          W
      US 1999-417197
                          Α3
                                19991007
L3
      ANSWER 32 OF 40
                        CAPLUS COPYRIGHT 2003 ACS on STN
      1998:378471 CAPLUS
ΑN
DN
      129:132071
      Regulation of the human p21/WAF1/Cip1 promoter in hepatic cells by
TT
     ***functional*** interactions between Sp1 and Smad family members Moustakas, Aristidis; Kardassis, Dimitris Division of Basic Sciences, School of Medicine, University of Crete,
CS
     Crete, 71110, Greece
Proceedings of the National Academy of Sciences of the United States of
S<sub>0</sub>
      America (1998), 95(12), 6733-6738
      CODEN: PNASA6; ISSN: 0027-8424
PB
      National Academy of Sciences
DT
     Journal
LA
     English
RE.CNT
         39
                THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 33 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      1998:32752
AN
                   CAPLUS
      128:178293
DN
TI
      The DAF-3 Smad protein antagonizes TGF-.beta.-related receptor signaling
      in the Caenorhabditis elegans dauer pathway
      Patterson, Garth I.; Koweek, Allison; Wong, Arthur; Liu, Yanxia; Ruvkun,
CS
     Department of Molecular, Harvard Medical School, Boston, MA, 02114, USA
     Genes & Development (1997), 11(20), 2679-2690
CODEN: GEDEEP; ISSN: 0890-9369
S0
PB
      Cold Spring Harbor Laboratory Press
      Journal
DT
     English
LA
RE.CNT 49
                THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 34 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     1997:732166 CAPLUS
DN
     128:10885
TI
     Increasing the level of expression of a foreign gene in eukaryotes using a
     nuclear retention signal and nuclear export factor
     Sedlacek, Hans Harald; Muller, Rolf; Luhrmann, Reinhard
IN
PΑ
     Hoechst Aktiengesellschaft, Germany
S<sub>0</sub>
     Eur. Pat. Appl., 41 pp.
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LA
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PΙ
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L9617851 A1 19971113 DE 1996-19617851 19960503
```

DE 19617851

```
19970501
     AU 9719982
                                             AU 1997-19982
                        Α1
                             19971106
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                                                               19970502
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                             19990106
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                                                               19970506
PRAI DE 1996-19617851 A
                             19960503
     ANSWER 35 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN 1997:567057 CAPLUS
L3
AN
     127:243372
DN
     Transforming growth factor (TGF-.beta.)-specific signaling by chimeric
TI
     TGF-.beta. type II receptor with intracellular domain of activin type IIB
     receptor
     Persson, Urban; Souchelnytskyi, Serhiy; Franzen, Petra; Miyazono, Kohei;
ΑU
     Ten Dijke, Peter; Heldin, Carl-Henrik
     Ludwig Institute for Cancer Research, Uppsala, S-751 24, Swed.
CS
     Journal of Biological Chemistry (1997), 272(34), 21187-21194
50
     CODEN: JBCHA3; ISSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
LA
L3
     ANSWER 36 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1994:694379 CAPLUS
AN
DN
     121:294379
TI
     A monomeric derivative of the cellular transcription factor CREB functions
     as a constitutive activator
AU
     Krajewski, Wladyslaw; Lee, Kevin A. W.
     Imp. Cancer Res. Fund, Clare Hall Lab., South Mimms, Hertfordshire, EN6
CS
     3LD, UK
     Molecular and Cellular Biology (1994), 14(11), 7204-10
S0
     CODEN: MCEBD4; ISSN: 0270-7306
     American Society for Microbiology
PR
DT
     Journal
     English
LA
L3
     ANSWER 37 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     1994:549708 CAPLUS
AN
DN
     121:149708
TI
     PML/RAR.alpha.+ U937 mutant and NB4 cell lines: retinoic acid restores the
     monocytic differentiation response to vitamin D3
ΑU
     Testa, Ugo; Grignani, Francesco; Barberi, Tiziano; Fagioli, Marta;
     Masciulli, Rosalba; Ferrucci, Pier Francesco; Seripa, Davide; Camagna,
     Antonio; Alcalay, Myrian; et al.
     Department of Hematology and Oncology, Istituto Superiore di Sanita, Rome,
CS
     Italy
SO
     Cancer Research (1994), 54(16), 4508-15
     CODEN: CNREA8; ISSN: 0008-5472
DT
     Journal
     English
LA
L3
     ANSWER 38 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1993:552114 CAPLUS
ΑN
DN
     119:152114
     Inhibitors of cell regulatory factors and methods for preventing or
TI
     reducing scarring
     Ruoslahti, Erkki I.; Longaker, Michael T.; Whitby, David J.; Harper, John
IN
     R.; Pierschbacher, Michael D.; Border, Wayne A.
     La Jolla Cancer Research Foundation, USA; University of California;
PA
     University of Utah
SO
     PCT Int. Appl., 73 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 6
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     wo 9309800
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```

AU 9331385 AU 673506

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```
EP 667784
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                                               ES 1992-925260
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US 1995-442063
     us 5654270
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     us 5705609
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     US 1992-882345
                         A2
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     us 1988-212702
                         В2
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                         В2
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     US 1992-865652
                         в1
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     us 1992-978931
                         В1
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     US 1994-303238
                         Α1
                              19940908
     US 1995-458834
                              19950602
                         Α1
L3
     ANSWER 39 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     1992:505095 CAPLUS
AN
DN
     117:105095
     Regulation of murine embryonic epithelial cell differentiation by
TI
                                ***growth***
                                                                   . ***beta***
        ***transforming***
                                                   ***factors***
     Gehris, Amy L.; Green, Robert M.
Jefferson Med. Coll., Thomas Jefferson Univ., Philadelpia, PA, 19107, USA
Differentiation (Berlin, Germany) (1992), 49(3), 167-73
AU
CS
S<sub>0</sub>
     CODEN: DFFNAW; ISSN: 0301-4681
DT
     Journal
     English
LA
L3
     ANSWER 40 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
AN
     1990:230385 CAPLUS
     112:230385
DN
       ***Functional***
                          receptors for ***transforming***
                                                                       ***growth***
TT
       ***factor*** -. ***beta*** . are retained by biochemically
     differentiated C2 myocytes in growth factor-deficient medium containing
     EGTA but down-regulated during terminal differentiation
     Hu, Jing Shan; Olson, Eric N.
M. D. Anderson Cancer Cent., Univ. Texas, Houston, TX, 77030, USA
ΑU
CS
     Journal of Biological Chemistry (1990), 265(14), 7914-19
S0
     CODEN: JBCHA3; ISSN: 0021-9258
DT
     Journal
     English
LA
=> D L4 1-27
L4
     ANSWER 1 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
ΑN
     2003:696617
                  CAPLUS
DN
     139:225485
     Methods for cloning, synthesis and purification of human growth hormone
TI
     and granulocyte colony stimulating factor in plants
IN
     Russell, Douglas A.; Schlittler, Michael
PA
SO
     U.S. Pat. Appl. Publ., 53 pp., Cont.-in-part of U.S. Ser. No. 316,847,
     abandoned.
     CODEN: USXXCO
DT
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LA
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ΡI
     US 2003167531
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                                               us 2001-824200
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     US 2002053094
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     US 2003033636
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     US 1999-316847
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```

US 2000-194217P

Р

```
ΑN
      2003:336102 CAPLUS
DN
      139:63517
TI
      Growth Factor-Binding Sequence in Human .alpha.2-Macroglobulin Targets the
      Receptor-Binding Site in ***

***Factor*** -. ***beta***
                                      ***Transforming***
                                                                  ***Growth***
      Arandjelovic, Sanja; Freed, Tiffany A.; Gonias, Steven L.
ΑU
      Departments of Pathology and Biochemistry and Molecular Genetics,
CS
     Charlottesville, VA, 22908, USA
Biochemistry (2003), 42(20), 6121-6127
CODEN: BICHAW; ISSN: 0006-2960
PR
      American Chemical Society
      Journal
DT
      English
LA
RE.CNT 59
                THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
      ANSWER 3 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
      2002:864122 CAPLUS
AN
DN
      138:71370
TI
      Converting nonhuman primate dendritic cells into potent antigen-specific
      cellular immunosuppressants by genetic modification
ΑU
      Asiedu, Clement; Pereboev, Alexander; Curiel, David T.; Dong, Sai Sai;
     Hutchings, Anne; Thomas, Judith M.
      Division of Transplantation Immunobiology, Department of Surgery,
CS
      University of Alabama at Birmingham, USĀ
      Immunologic Research (2002), 26(1-3), 297-302
SO
      CODEN: IMRSEB; ISSN: 0257-277X
PB
     Humana Press Inc.
      Journal; General Review
DT
LA
      English
                THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 30
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 4 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2002:742821 CAPLUS
AN
DN
      138:71843
      Rhesus monocyte-derived dendritic cells modified to over-express
TI
      TGF-.beta.1 exhibit potent veto activity
     Asiedu, Clement; Dong, Sai S.; Pereboev, Alexander; Wang, Weila; Navarro, Jesus; Curiel, David T.; Thomas, Judith M.
ΑU
CS
      Division of Transplant Immunology, Department of Surgery, University of
     Alabama at Birmingham, Birmingham, AL, USA Transplantation (2002), 74(5), 629-637
SO
     CODEN: TRPLAU; ISSN: 0041-1337
PB
      Lippincott Williams & Wilkins
      Journal
DT
LA
      English
RE.CNT 38
                THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L4
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AN
      2001:748023 CAPLUS
      135:314414
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     Expression and purification of bioactive, authentic human growth hormone and granulocyte colony stimulating factor in plants
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      Russell, Douglas; Schlittler, Michael
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LA
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```

```
AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
-194217P P 20000403
PRAI US 2000-194217P
      WO 2001-US10765
                                 20010403
                           W
L4
      ANSWER 6 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2001:125225 CAPLUS
AN
      134:309568
DN
      Blockade of TGF-.beta. signaling in T cells prevents the development of
TI
      experimental glomerulonephritis
      Kanamaru, Yutaka; Nakao, Atsuhito; Mamura, Mizuko; Suzuki, Yusuke; Shirato, Isao; Okumura, Ko; Tomino, Yasuhiko; Ra, Chisei Allergy Research Center, Division of Nephrology, School of Medicine,
CS
      Juntendo University, Tokyo, 113-8421, Japan
      Journal of Immunology (2001), 166(4), 2818-2823
50
      CODEN: JOIMA3; ISSN: 0022-1767
PR
      American Association of Immunologists
      Journal
DT
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LA
RE.CNT
        31
                THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 7 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2000:856739 CAPLUS
AN
      134:37538
DN
TI
      A 16-amino acid peptide from human .alpha.2-macroglobulin binds
        ***transforming*** ***growth***
                                                       ***factor*** -. ***beta***
      and platelet-derived growth factor-BB
     Webb, Donna J.; Roadcap, David W.; Dhakephalkar, Anita; Gonias, Steven L. Departments of Pathology, Biochemistry, University of Virginia School of Medicine, Charlottesville, VA, 22908, USA Protein Science (2000), 9(10), 1986-1992
ΔIJ
CS
50
      CODEN: PRCIEI; ISSN: 0961-8368
PB
      Cambridge University Press
      Journal
DT
      English
LA
RE.CNT
        35
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L4
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AN
      1999:392621 CAPLUS
DN
      131:54753
      Expression of
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TI
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      cytoplasm without leader sequences
      Mascarenhas, Desmond; Zhang, Yang; Olson, Pamela S.; Olsen, David R.;
ΙN
      Cohen, Pedro A.; Nguyen, Kimyen B.
PA
      Celtrix Pharmaceuticals, Inc., USA
      U.S., 80 pp., Cont.-in-part of U.S. 5,629,172.
S0
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FAN.CNT 3
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                THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 58
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
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      ANSWER 9 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1999:274814
ΑN
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      131:57268
ΤI
      TGF-.beta.1 in liver fibrosis: an inducible transgenic mouse model to
      study liver fibrogenesis
      Kanzler, Stephan; Lohse, Ansgar W.; Keil, Andrea; Henninger, Jurgen;
      Dienes, Hans P.; Schirmacher, Peter; Rose-John, Stefan; Buschenfelde, Karl
      H. Meyer Zum; Blessing, Manfred
      Boehringer Ingelheim Research Group, and 2First Department of Medicine,
CS
     University of Mainz, Mainz, 55101, Germany
American Journal of Physiology (1999), 276(4, Pt. 1), G1059-G1068
SO
```

CODEN: AJPHAP; ISSN: 0002-9513 American Physiological Society

PB

```
English
RE.CNT 62
                 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD
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      1998:352861 CAPLUS
AN
DN
      129:50102
      Nucleotide and protein sequences of liver activin/inhibin and and their
TI
      therapeutic activities
Bonadio, Jeffrey; Fang, Jianming
Regents of the University of Michigan, USA
IN
PA
50
      PCT Int. Appl., 143 pp.
      CODEN: PIXXD2
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                                 19980528
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      ANSWER 11 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1997:544772 CAPLUS
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      127:243767
DN
      Capture and expansion of bone marrow-derived mesenchymal progenitor cells
TI
      with a ***transforming*** ***growth*** ***factor***
      ***beta*** .1-von Willebrand's factor ***fusion*** protein for retrovirus-mediated delivery of coagulation factor IX
Gordon, Erlinda M.; Skotzko, Michael; Kundu, Ramendra Krishna; Han, Bo;
ΑU
      Andrades, Jose; Nimni, Marcel; Anderson, W. French; Hall, Frederick L.
      Gene Therapy Laboratories, Childrens Hospital Los Angeles, Los Angeles,
CS
      CA, 90033, USA
SO
      Human Gene Therapy (1997), 8(11), 1385-1394
      CODEN: HGTHE3; ISSN: 1043-0342
PB
      Liebert
DT
      Journal
      English
LA
      ANSWER 12 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
      1997:474561 CAPLUS
AN
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      127:131561
                                  ***growth***
TI
        ***Transforming***
                                                        ***factor*** -. ***beta***
      regulates transdifferentiation of medial edge epithelium during palatal
        ***fusion*** and associated degradation of the basement membrane
ΑU
      Kaartinen, Vesa; Cui, Xiao-Mei; Heisterkamp, Nora; Groffen, John; Shuler.
      Charles F.
     Department of Pathology, Childrens Hospital Los Angeles Research Institute, Los Angeles, CA, USA
Developmental Dynamics (1997), 209(3), 255-260
CS
SO
      CODEN: DEDYEI; ISSN: 1058-8388
      Wiley-Liss
PB
DT
      Journal
      English
LA
      ANSWER 13 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
      1997:341952 CAPLUS
ΑN
DN
      126:313187
```

Recombinant expression of protein of interest as \*\*\*fusion\*\*\*

with interleukin-1-like protein or leader-peptide-deleted-translocating

TI

```
ΙN
     Mascarenhas, Desmond; Zhang, Yang; Olson, Pamela S.; Olsen, David R.;
     Cohen, Pedro A.
     Celtrix Pharmaceuticals, Inc., USA
U.S., 77 pp., Cont.-in-part of U.S. Ser. No. 100,744.
PA
50
      CODEN: USXXAM
DT
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     English
LA
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L4
     ANSWER 14 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1997:182887
AΝ
                   CAPLUS
DN
     126:236690
TI
     Type I collagen combined with a recombinant TGF-.beta. serves as a
     scaffold for mesenchymal stem cells
     Andrades, Jose A.; Nimni, Marcel E.; Han, Bo; Ertl, Delia C.; Hall,
     Frederick L.; Becerra, Jose
Department of Cell Biology and Genetics, Faculty of Sciences, University
CS
     of Malaga, Malaga, 29071, Spain
SO
     International Journal of Developmental Biology (1996), (Suppl. 1,
     Proceedings of the First Congress of the Spanish Society of Developmental
     Biology, 1996), 107s-108s
CODEN: IJDBE5; ISSN: 0214-6282
University of the Basque Country Press
PB
DT
     Journal
     English
ΙA
L4
     ANSWER 15 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
     1997:182767 CAPLUS
ΑN
DN
     126:272449
     Latent ***transforming***
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                                        ***growth***
                                                            ***factor***
        ***beta*** . binding protein domains involved in activation and
     transglutaminase-dependent crosslinking of latent ***growth*** ***factor*** -. ***beta*** .
                                                                ***transforming***
     Nunes, Irene; Gleizes, Pierre-Emmanuel; Metz, Christine N.; Rifkin, Daniel
ΑU
CS
     Department of Cell Biology, Kaplan Cancer Center, New York University
     Medical Center, New York, NY, 10016, USA
Journal of Cell Biology (1997), 136(5), 1151-1163
SO
     CODEN: JCLBA3; ISSN: 0021-9525
PB
     Rockefeller University Press
DT
     Journal
     English
L4
     ANSWER 16 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
     1995:479799 CAPLUS
AN
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     122:236790
     Hepatic expression of ***mature***
                                                  ***transforming***
TI
        ***growth*** ***factor***
                                              ***beta*** .1 in transgenic mice
     results in multiple tissue lesions
ΑU
     Sanderson, Nancy; Factor, Valentina; Nagy, Peter; Kopp, Jeffrey; Kondaiah,
     Paturu; Wakefield, Lalage; Roberts, Anita B.; Sporn, Michael B.;
     Thorgeirsson, Snorri S.
CS
     National Institute of Dental Research, National Institutes of Health,
     Bethesda, MD, 20892, USA
Proceedings of the National Academy of Sciences of the United States of
SO
     America (1995), 92(7), 2572-6
CODEN: PNASA6; ISSN: 0027-8424
PB
     National Academy of Sciences
DT
     Journal
     English
LA
L4
     ANSWER 17 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1994:549708 CAPLUS
AN
     121:149708
```

PML/RAR.alpha.+ U937 mutant and NB4 cell lines: retinoic acid restores the

DN

TI

```
ΑU
      Testa, Ugo; Grignani, Francesco; Barberi, Tiziano; Fagioli, Marta;
      Masciulli, Rosalba; Ferrucci, Pier Francesco; Seripa, Davide; Camagna,
      Antonio; Alcalay, Myrian; et al.
CS
      Department of Hematology and Oncology, Istituto Superiore di Sanita, Rome,
SO
      Cancer Research (1994), 54(16), 4508-15
      CODEN: CNREA8; ISSN: 0008-5472
      Journal
DT
      English
LA
L4
      ANSWER 18 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1992:401809 CAPLUS
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      117:1809
DN
        ***Transforming***
                                 ***growth***
                                                    ***factor*** -. ***beta***
TI
                                                                                        .3
      (TGF-.beta.3) detection and inhibition, antibodies to TGF-.beta.3, and
      pharmaceutical compositions containing the pro region of TGF-.beta.3
IN
      Iwata, Kenneth K.; Foulkes, J. Gordon; Ten Dijke, Peter; Haley, John D.
      Oncogene Science, Inc., USA
PA
S<sub>0</sub>
      PCT Int. Appl., 98 pp.
      CODEN: PIXXD2
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      US 1986-847931
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      US 1986-922121
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L4
AN
      1992:38680 CAPLUS
DN
      116:38680
TI
      Desmin is present in proliferating rat muscle satellite cells but not in
      bovine muscle satellite cells
     Allen, Ronald E.; Rankin, Lucinda L.; Greene, Elizabeth A.; Boxhorn, Linda K.; Johnson, Sally E.; Taylor, Richard G.; Pierce, Paul R. Dep. Anim. Sci., Univ. Arizona, Tucson, AZ, 85721, USA Journal of Cellular Physiology (1991), 149(3), 525-35
ΑU
CS
S<sub>0</sub>
      CODEN: JCLLAX; ISSN: 0021-9541
DT
      Journal
LA
      English
L4
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AN
      1991:672656 CAPLUS
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                     ***transforming***
ΤI
      Recombinant
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        ***beta*** . analogs
      Cohen, Charles M.
IN
PA
      Creative Biomolecules, Inc., USA
SO
      PCT Int. Appl., 43 pp.
      CODEN: PIXXD2
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```

wo 1990-us6006

19901018

PΙ

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19910502

```
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CA 2070393 AA 19910419 CA 1990-2070393 19901018
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AN
     115:175892
DN
     Inhibiting and stimulating effects of TGF-.beta.1 on osteoclastic bone
TI
     resorption in fetal mouse bone organ cultures
     Dieudonne, S. C.; Foo, P.; Van Zoelen, E. J. J.; Burger, E. H.
ΑU
     Acad. Cent. Dent., Vrije Univ., Amsterdam, 1081 BT, Neth.
C$
     Journal of Bone and Mineral Research (1991), 6(5), 479-87
50
     CODEN: JBMREJ; ISSN: 0884-0431
DT
     Journal
LA
     English
L4
     ANSWER 22 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1991:528526 CAPLUS
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     115:128526
     Tissue-derived tumor growth inhibitors, methods of preparation, and uses
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IN
     Iwata, Kenneth K.; Stephenson, John R.; Ten Dijke, Peter; Franco, Robert;
     Gold, Leslie I.; Foulkes, J. Gordon
PΔ
     Oncogene Science, Inc., USA
S0
     PCT Int. Appl., 190 pp.
     CODEN: PIXXD2
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AN
     1991:486162 CAPLUS
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     115:86162
     Secretion and transcriptional regulation of ***transforming***

***growth*** ***factor*** -. ***beta*** .3 during myogenesis

Lafyatis, Robert; Lechleider, Robert; Roberts, Anita B.; Sporn, Michael B.

Lab. Chemoprev., Natl. Cancer Inst., Bethesda, MD, 20892, USA

Molecular and Cellular Biology (1991), 11(7), 3795-803
TI
ΑU
CS
50
     CODEN: MCEBD4; ISSN: 0270-7306
DT
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     ANSWER 24 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
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     1991:1783 CAPLUS
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DN
     114:1783
     Cloning and expression of ***transforming***
TI
                                                                ***growth***
        Purchio, Anthony F.; Madisen, Linda; Webb, Nancy
IN
PA
     Oncogen, L. P., USA
     Eur. Pat. Appl., 58 pp.
50
     CODEN: EPXXDW
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```

PΙ

EP 376785

Α2

19900704

19891214

EP 1989-403480

```
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620 A 19930622 US 1989-446020 198
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L4
     ANSWER 25 OF 27
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     1990:31707 CAPLUS
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DN
     Cloning and expression of the gene for transforming growth factor B-2 in
TI
     mammalian cells
     Purchio, Anthony F.; Madisen, Linda; Webb, Nancy
IN
PA
     Oncogen, USA
     Fr. Demande, 59 pp.
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     ANSWER 26 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
     1989:109071 CAPLUS
AN
DN
     110:109071
     Regulation of skeletal muscle satellite cell proliferation and differentiation by ***transforming*** ***growth***
TI
                                                                       ***factor***
                     , insulin-like growth factor I, and fibroblast growth
     Allen, Ronald E.; Boxhorn, Linda K.
ΑU
```

Dep. Anim. Sci., Univ. Arizona, Tucson, AZ, 85721, USA Journal of Cellular Physiology (1989), 138(2), 311-15

CS SO

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Maximum Match 100%

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17: em hum:\*

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19: em mu:\*

20: em om:\*

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REFERENCE
            Strober, W., Nakamura, K., Kitani, A. and Fuss, I.J.
  AUTHORS
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ACCESSION
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VERSION
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          Polymorphism in the porcine transforming growth factor beta 1 gene
 TITLE
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          cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
          Evidence for alternate splicing and polyadenylation
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          J. Biol. Chem. 263 (34), 18313-18317 (1988)
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VERSION
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           Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
              (bases 1 to 1605)
           Derynck, R. and Rhee, L.
 AUTHORS
 TITLE
           Sequence of the porcine transforming growth factor-beta precursor
 JOURNAL
           Nucleic Acids Res. 15 (7), 3187 (1987)
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          X12373
ACCESSION
VERSION
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KEYWORDS
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REFERENCE
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 AUTHORS
          Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
          Nucleotide sequence of chicken transforming growth factor-beta 1
 TITLE
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 JOURNAL
          Nucleic Acids Res. 16 (17), 8730 (1988)
          88335639
 MEDLINE
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REFERENCE
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 AUTHORS
          Jakowlew, S.B.
 TITLE
          Direct Submission
          Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
 JOURNAL
          health, National Cancer Institute, Laboratory of Chemoprevention,
          Building 41, Room B902, Bethesda, Maryland 20892, USA
COMMENT
          The submitters believe that the chicken cDNA library was
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REFERENCE
 AUTHORS
          Woodall, C.J., McLaren, L.J. and Watt, N.J.
 TITLE
          Sequence and chromosomal localisation of the gene encoding ovine
          latent transforming growth factor-beta 1
 JOURNAL
          Gene 150 (2), 371-373 (1994)
          95121932
 MEDLINE
          7821809
  PUBMED
REFERENCE
             (bases 1 to 1173)
 AUTHORS
          Woodall, C.
 TITLE
          Direct Submission
 JOURNAL
          Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
          Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
          Edinburgh EH9 IQH, UK
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ACCESSION
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VERSION
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SOURCE
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REFERENCE
             (bases 1 to 1369)
 AUTHORS
          Manning, A.M., Auchampach, J.A., Drong, R.F. and Slightom, J.L.
 TITLE
          Cloning of a canine cDNA homologous to human transforming growth
           factor-beta 1 (TGFbeta1)
 JOURNAL
          Unpublished (1994)
COMMENT
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REFERENCE AUTHORS	C 1	ammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; ercopithecinae; Cercopithecus. (bases 1 to 1561) harples,K., Plowman,G.D., Rose,T.M., Twardzik,D.R. and	

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          Cloning and sequence analysis of simian transforming growth
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         DNA 6 (3), 239-244 (1987)
 JOURNAL
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Purchio, A.F.

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VERSION
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  AUTHORS
            Strausberg, R.
            Direct Submission
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  JOURNAL
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
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COMMENT
            Contact: MGC help desk
            Email: cqapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:
                            http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.
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ORGANI		Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REMARK COMMENT		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk

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          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
          info@bcgsc.bc.ca
          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
          Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
          Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
          Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
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Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

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RESULT 11 BC001180

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ACCESSION BC001180

VERSION BC001180.1 GI:12654682

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1780)

AUTHORS Strausberg, R.
TITLE Direct Submission

JOURNAL Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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VERSION
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 AUTHORS
           Ohashi, H., Ishii, Y., Miyata, Y., Miyazono, K., Miyagawa, K. and
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           PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION
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REFERENCE
 AUTHORS
          Riku, M.A.D.D. and Debitsudo, B.G.
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          Patent: JP 1986219395-A 1 29-SEP-1986;
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## RESULT 15 BT007245

linear PRI 13-MAY-2003 LOCUS BT007245 1173 bp mRNA DEFINITION Homo sapiens transforming growth factor, beta 1 (Camurati-Engelmann disease) mRNA, complete cds.

ACCESSION BT007245

VERSION BT007245.1 GI:30583328

KEYWORDS FLI\_CDNA.

SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 1173)
 AUTHORS
            Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
            Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
            Phelan, M. and Farmer, A.
  TITLE
            Cloning of human full-length CDSs in BD Creator(TM) System Donor
            vector
  JOURNAL
            Unpublished
               (bases 1 to 1173)
REFERENCE
 AUTHORS
            Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
            Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
            Phelan, M. and Farmer, A.
  TITLE
            Direct Submission
            Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
  JOURNAL
            Circle, Palo Alto, CA 94303, USA
            This CDS clone is a part of a collection of human full length
COMMENT
            expression clones generated by BD Biosciences Clontech and the
            Harvard Institute of Proteomics. Each CDS has been cloned in two
            forms: with and without stop-codon (to allow fusion with C-terminal
            tag). The CDS has been directionally cloned using BD In-Fusion(TM)
            cloning system between the Sall and HindIII sites of the pDNR-DUAL
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Job time : 4678.52 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 359.617 Seconds

(without alignments)

8985.201 Million cell updates/sec

Title: US-10-017-372E-8

Perfect score: 1197

Sequence: 1 atggcgccttcggggctgcg.....gttcctgcaagtgcagctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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## SUMMARIES

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2	958.2	80.1	2742	22	AAI58342	Human polynucleoti
3	956.6	79.9	1559	13	AAQ20289	Sequence encoding
4	956.6	79.9	1561	11	AAQ03268	Simian transformin
5	956.6	79.9	1821	12	AAQ13392	Human pro-TGF-beta
6	956.6	79.9	2537	7	AAN60972	Sequence encoding
7	956.6	79.9	2537	11	AAQ03301	cDNA encoding huma
8	956.6	79.9	2537	11	AAQ02814	Sequence of pre-TG
9	956.6	79.9	2537	17	AAT15720	Pre-transforming g
10	955	79.8	2527	25	ABQ76674	Androgen receptor
11	955	79.8	2537	15	AAQ56923	Human pre-TGF-beta
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13	953.4	79.6	1560	11	AAQ03508	Simian Transformin
14	951.8	79.5	2537	19	AAV52933	Human pre-transfor
15	945.2	79.0	1176	25	ABV75391	TGFB1 Arg25Pro pol
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20	943.6	78.8	1176	25	ABV75392	TGFB1 Arg25Pro pol
21	943.6	78.8	1303	11	AAQ09317	Monkey transformin
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     Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
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     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
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KW
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    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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    Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
    WPI; 2002-026155/03.
    P-PSDB: AAE13596.
DR
XX
PT
    Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
    disease in humans, comprises vector containing transforming growth
PT
    factor-beta under the control of inducible promoter -
XX
PS
    Claim 1; Fig 1; 78pp; English.
XX
CC
    The invention relates to a composition containing a vector comprising a
CC
    gene encoding a regulatory transcription factor under the control of a
CC
    promoter encoding a transforming growth factor-beta (TGF-beta). The
CC
    vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC
    or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
    is part of a host suspected of having an autoimmune disease, especially
CC
    inflammatory bowel disease (IBD), under conditions such that the
CC
    polypeptide encoded by the nucleic acid sequence in the vector is
CC
    expressed. The vector is delivered using a delivery system. The delivery
CC
    of the vector results in substantial elimination of symptoms of the
CC
    autoimmune disease and increased production of IL-10 by the host. The
CC
    composition is useful for treating various diseases with an autoimmune
    component such as multiple sclerosis, rheumatoid arthritis, systemic
CC
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
CC
    The vector is further useful for screening of the effect of test
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
CC
    The present sequence is a cDNA encoding porcine TGF-betal mutant.
XX
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            256 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 315
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Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360	
Db	316	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 375	
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Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480	
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Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540	
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Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600	
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QУ	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660	
Db	616	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 675	
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720	
Db	676	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 735	
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Db	736	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 795	
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840	
Db	796	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA 849	
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900	
Db	850		
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960	
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Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020	
Db	952		
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Db	1012	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGC	
Qy	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140	
Db	1072		

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1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
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RESULT 2
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XΧ
AC
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ХX
DT
     22-OCT-2001 (first entry)
XX
     Human polynucleotide SEQ ID NO 545.
DE:
XX
KW
     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
     peripheral nervous system; neuropathy; central nervous system; CNS;
KW
     Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW
KW
     amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW
     chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW
     leukaemia; ss.
XX
OS
     Homo sapiens.
XX
PN
    WO200153312-A1.
XX
PD
     26-JUL-2001.
XX
     26-DEC-2000; 2000WO-US34263.
PF
XX
PR
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
PR
     09-JUL-2000; 2000US-0598042.
PR
     19-JUL-2000; 2000US-0620312.
PR
     03-AUG-2000; 2000US-0653450.
     14-SEP-2000; 2000US-0662191.
PR
     19-OCT-2000; 2000US-0693036.
PR
PR
     29-NOV-2000; 2000US-0727344.
XX
PΑ
     (HYSE-) HYSEQ INC.
XX
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PΙ
     Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y,
                                                           Zhang J;
PΙ
     Zhao QA, Zhou P, Goodrich R, Drmanac RT;
PΙ
XX
DR
     WPI; 2001-442253/47.
     P-PSDB; AAM39186.
DR
XX
PT
     Novel nucleic acids and polypeptides, useful for treating disorders
PT
     such as central nervous system injuries -
XX
     Claim 1; SEQ ID NO 545; 10078pp; English.
PS
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
```

```
CC
   system, such as peripheral nervous injuries, peripheral neuropathy and
CC
   localised neuropathies and central nervous system diseases, such as
CC
   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC
   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
   utilisation of the activities such as: Immune system suppression,
CC
   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC
   assays for receptor activity, arthritis and inflammation, leukaemias and
CC
   C.N.S disorders.
CC
   Note: The sequence data for this patent did not form part of the printed
CC
   specification.
XX
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 Best Local Similarity
                   88.6%; Pred. No. 1.6e-193;
 Matches 1060; Conservative
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                                                24; Gaps
                                                          1;
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          902 CTGACGCCTGGCCGGCCGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
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       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
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          - -
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Qу
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Db
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Qу
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of the invention may be used to treat diseases of the peripheral nervous

CC

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Db
      1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
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QУ
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
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Qу
          Db
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       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
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Qу
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Db
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Qу
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Db
Qу
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Db
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Db
RESULT 3
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ID
XX
AC
   AAQ20289;
XX
DT
   25-MAR-2003 (updated)
DT
   16-APR-1992 (first entry)
XX
DE
   Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW
   Hypertension therapy; hypotensive agent; blood pressure modulator;
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KW

XX

SS.

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OS
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XX
    20-JUN-1991;
PF
               91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
PA
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PΙ
    Oleson FB, Comereski CR;
XX
    WPI; 1992-024199/03.
DR
    P-PSDB; AAR20124.
DR
XX
РТ
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-betal/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
 Query Match
                      79.9%; Score 956.6; DB 13; Length 1559;
 Best Local Similarity 88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative 0; Mismatches 114; Indels
                                                      24; Gaps
                                                                  1;
QУ
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Qу
            Db
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        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Ov
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Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGCCC	500
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGGGGGGGGG	560
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	561	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qу	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	621	TATGACAAGTTCAAGCAGAGCACACACACACATCATATATAT	680
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Db		TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	
QУ		ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	
Db		ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	
QУ			720
Db		GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
Qy -		TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	
Db		ACCGGCCGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	
Qy		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	
QУ	1095	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	
Db	10,5		
QУ		TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	
		TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	
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ID
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XX
                (updated)
DT
    25-MAR-2003
DT
    12-AUG-1990 (first entry)
XX
    Simian transforming growth factor-beta cDNA.
DE
XX
    Transforming growth factor-beta; psoriasis; TGF-beta; ss.
KW
XX
OS
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                88US-0229133.
PR
XX
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PΑ
XX
PΙ
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
    WPI; 1990-038499/06.
DR
DR
    P-PSDB; AAR03743.
XX
    Inhibition of proliferation of epidermal cells -
PT
    used to treat psoriasis by contacting cells with compositions
    containing transforming growth factor-beta.
PT
XX
    Disclosure; fig 1; 20pp; English.
PS
```

```
XX
   TGF-beta may be used in the treatment of hyperplasia
CC
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
   induced phenomena. See also AAQ03269 and AAR03750.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ
   Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
 Query Match
                  79.9%; Score 956.6; DB 11; Length 1561;
 Best Local Similarity 88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative
                      0; Mismatches 114;
                                      Indels
                                             24: Gaps
                                                       1;
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Qу
          Db
       322 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 381
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Qy
          382 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 441
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DT
   20-NOV-1991 (first entry)
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DΕ
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XX
KW
   Osteogenetic; tumoricidal; ss.
XX
OS
   Homo sapiens.
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FT

misc RNA

599..1684

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ХX
PR
   07-DEC-1989;
              89JP-0318243.
XX
PΑ
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XX
DR
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   P-PSDB; AAR13813.
DR
XX
PT
   Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
РТ
   preparing DNA chain contq. base sequence coding for human
PT
   pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
   Claim 1; Fig 1; 16pp; Japanese.
XX
CC
   The DNA sequence encodes human prepro-TGF-beta 1 which can be
CC
   produced by recombinant methods, it has osteogenetic and
CC
   tumoricidal activity.
XX
SO
   Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
 Query Match
                    79.9%;
                         Score 956.6; DB 12; Length 1821;
 Best Local Similarity
                   88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative
                        0; Mismatches 114;
                                         Indels
                                                24; Gaps
                                                           1;
         Qу
           Db
       61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGGTG 120
Qу
           Db
       572 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 631
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          Db
       632 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTGGCC 691
Qу
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
           Db
       692 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 751
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          752 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 811
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
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Db	812	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	871
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	872	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	931
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	991
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1051
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1052	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1111
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1112	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1171
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1172	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1231
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1232	ACCGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1291
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1292	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1345
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1346		1387
Qу	901	TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1388	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1447
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1448	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1507
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1508	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1567
Qy	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1568	GCGCCGTGCTGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	1627
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	97
Db	1628	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 168	34

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RESULT 6
AAN60972
     AAN60972 standard; cDNA; 2537 BP.
XX
AC
     AAN60972;
XX
DT
     31-OCT-2002 (updated)
DT
     28-OCT-1991 (first entry)
XX
DΕ
     Sequence encoding preTGF-beta.
XX
KW
     Transforming growth factor beta; cancer; wound healing.
XX
OS
     Unidentified.
XX
FΗ
     Key
                     Location/Qualifiers
FT
     misc structure 37..113
FT
                     /*tag= a
FT
                     /note= "Sequence can form stable hairpin loops"
FT
     CDS
                     842..2014
FT
                     /*tag= b
FT
     mat peptide
                     1676..2011
FT
                     /*tag= c
XX
ΡN
     EP200341-A.
XX
PD
     10-DEC-1986.
XX
PF
     21-MAR-1986;
                    86EP-0302112.
XX
PR
     22-MAR-1985;
                   85US-0715142.
     13-MAR-1987;
PR
                    87US-0025423.
XX
PΑ
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA;
XX
     WPI; 1986-326875/50.
DR
DR
     P-PSDB; AAP61468.
XX
     TGF-beta prodn. from transformed hosts - useful esp. for treating
PΤ
PΤ
     wounds (J6 2/9/86).
XX
PS
     Disclosure; Fig 1b; 26pp; English.
XX
CC
     The gene product is known to stimulate cell proliferation and
CC
     inhibit anchorage-dependent growth of a variety of human cancer cell
CC
     lines, it is esp. useful in treatment of burns and the promotion of
CC
     surface and internal wound healing. TGF-beta may be expressed from a
CC
     transformed CHO cell line.
CC
     (Updated on 31-OCT-2002 to add missing OS field.)
XX
SO
     Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
  Query Match
                          79.9%; Score 956.6; DB 7; Length 2537;
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			Similarity 9; Conserva					Indels	24;	Gaps	1;
Qу		1	ATGGCGCCTTC								60
Db		842	 ATGCCGCCCTC								901
Qу		61	CTGACGCCTGG								120
Db		902	CTGACGCCTGG		 			 AGACTATO			961
Qу		121	GTGAAGCGGAA								180
Db		962	GTGAAGCGGAA		 						1021
Qу		181	AGCCCCCGAG		 					GCTCTT	240
Db	1	022	AGCCCCCGAG		 					GCCCTG	1081
Qу		241	TACAACAGTAC		 						300
Db	1	082	TACAACAGCAC		 						1141
Qу		301	GCGGACTACTA							_	360
Db	1	142	GCCGACTACTA		 						1201
Qу		361	TATGATAAATT		 CCACAG	_		IGTTCAAC		GAGCTC	420
Db	1	202	TATGACAAGTT		 					GAGCTC	1261
Qу		421	CGGGAAGCGGT								480
Db	1	262	CGAGAAGCGGT		 						1321
Qу		481	AAGTTAAAAGT						GATTCC		540
Db	1	.322	AAGTTAAAAGT		 						1381
Qу		541	TACCTCAGCAA								600
Db	1	.382	TACCTCAGCAA		 						1441
Qу		601	ACCGGAGTTGT		 rgacccg(	CAGAGA	AGGCTA'	ragagggi 	TTTCGC	CTCAGT	660
Db	1	442	ACCGGAGTTGT		 rgagccg'	TGĠĀĠŒ		TGAGGG	CTTTCGC	CTTAGC	1501
Qу		661	GCCCACTCTTC								720
Db	1	502	GCCCACTGCTC								1561
Qу		721	TCTGGCCGCCG		 CACCAT		GCATGA	ACCGGCCC	TTCCTG	CTCCTC	780
Db	1	562	ACCGGCCGCCG		 		GCATGA	ACCGGCCT	TTCCTG	CTTCTC	1621
Qу		781	ATGGCCACCCC	CGCTGGAGA						GACTAC	840

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841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
QУ
                          Db
       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
QУ
           Db
       1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Dh
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
           1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
           1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           Db
       1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 7
AA003301
    AAQ03301 standard; DNA; 2537 BP.
XX
   AAQ03301;
AC
XX
DT
    25-MAR-2003
               (updated)
DT
    05-AUG-1990 (first entry)
XX
    cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
DΕ
DΕ
XX
KW
    Transforming growth factor-beta-1 (TGF-beta-1);
    neoplastic cell line inhibition;
KW
    EGF-potentiated anchorage-independent growth;
KW
XX
OS
    Homo sapiens.
XX
                 Location/Qualifiers
FΗ
    Key
FT
    CDS
                 842..2014
FT
                 /*tag= a
                 1676..2011
FT
   mat peptide
FT
                 /*tag=b
    misc difference 37..113
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FT
                 /note="stable hairpin loops"
FT
    misc feature
                 2015..2100
FT
                 /*tag=d
                 /note="G-C rich sequence
FT
FT
                  and a downstream TATA-like sequence"
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1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675

Db

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ΡN
   US4886747-A.
XX
PD
   12-DEC-1989.
XX
ΡF
   13-MAR-1987:
              87US-0025423.
XX
PR
   13-MAR-1987; 87US-0025423.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
   Derynck RMA, Goeddel DV;
XX
DR
   WPI; 1990-051338/07.
   P-PSDB; AAR05258.
DR
XX
PΤ
   Nucleic acid encoding transforming growth factor-beta -
PΤ
   cloned into expression vectors for expression in eukaryotic host
PT
   cells for therapeutic use
XX
PS
   Disclosure; Fig 1b; 28pp; English.
XX
CC
   It was obtained by an analysis of several overlapping cDNAs and gene
CC
   fragments, leading to the detn. of a continuous sequence corresp. to the
   TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
CC
CC
   encode biologically active transforming growth factor (TGF-beta),
CC
   operably linked to DNA that encodes a secretory leader (SL). It, or a
CC
   nucleic acid capable of hybridising with it, can also be labelled and
CC
   used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
CC
   proteins.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
   Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                    79.9%; Score 956.6; DB 11; Length 2537;
 Query Match
                    88.5%; Pred. No. 3.5e-193;
 Best Local Similarity
 Matches 1059; Conservative
                        0; Mismatches 114; Indels 24; Gaps
                                                           1;
         Qу
           Db
       61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           Db
       902 CTGACGCCTGGCCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
           Db
       962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
       181 AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141
Db
```

XX

Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142		1201
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676		1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1778	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1837
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1838	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1897
Qу	1081	GCGCCGTGCTGCGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1898	GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	1957

```
Qу
        1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
             Db
        1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 8
AAQ02814
    AAQ02814 standard; cDNA; 2537 BP.
XX
AC
    AAQ02814;
XX
DT
    25-MAR-2003 (updated)
DT
    31-OCT-2002 (updated)
DT
    31-MAY-1989 (first entry)
XX
DΕ
    Sequence of pre-TGF-betal cDNA.
XX
KW
    Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
    inhibition.
XX
OS
    Homo sapiens.
XX
FΗ
                    Location/Qualifiers
    Key
FT
                    842..2011
    CDS
FT
                    /*taq=a
FT
                    /label=pre-TGF beta 1
FT
    CDS
                    1677..2011
FT
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                    /label=mature TGF-beta 1
FT
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FT
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FT
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                    863..911
FT
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FT
XX
ΡN
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XX
    14-DEC-1989.
PD
XX
ΡF
    08-JUN-1988;
                  88WO-US01945.
XX
PR
    08-JUN-1988;
                   88WO-US01945.
XX
     (GETH ) GENENTECH INC.
PA
XX
    Dernyck RMA, Goeddel DV;
PΙ
XX
    WPI; 1990-007474/01.
DR
    P-PSDB; AAR04034.
DR
XX
    Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT
```

probe, or to produce TGF beta 3, for growth inhibition of certain normal

PT

```
and neoplastic cells, eq A549.
XX
PS
   Disclosure; Fig. 1b; 61pp; English.
XX
CC
   Sequence encodes the 390 amino acid (AA) precursor transforming growth
    factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
CC
    the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
CC
   potential secondary structure. The TATA-like sequence in the 3' untrans-
CC
CC
    lated region of the gene is presumably a polyadenylation signal. Mature
CC
   TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
CC
    cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
CC
    acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a
CC
   probe or to produce TGF-beta 3 for inhibition of growth of normal and
CC
   neoplastic cells.
    (Updated on 31-OCT-2002 to add missing OS field.)
CC
CC
    (Updated on 25-MAR-2003 to correct PR field.)
    (Updated on 25-MAR-2003 to correct PI field.)
CC
XX
SQ
   Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                    79.9%; Score 956.6; DB 11; Length 2537;
                    88.5%; Pred. No. 3.5e-193;
 Best Local Similarity
 Matches 1059: Conservative
                        0; Mismatches 114; Indels
                                                 24; Gaps
                                                           1:
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           902 CTGACGCCTGCCCGCCGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Dh
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
QУ
      Db
Qу
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
           Db
       1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
       361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
           Db
       1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
           1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Ov
```

PT

```
Db
      1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
Qу
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
          1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
Db
QУ
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
Оy
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
          Db
      1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACTGCAAGTGGACATCAACGGGTTCACT 1561
Qу
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
           1562 ACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
Db
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          Db
      1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
       841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Dh
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
          1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
      1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 9
   AAT15720 standard; cDNA; 2537 BP.
ΙD
XX
AC
   AAT15720;
ХX
DT
   25-MAR-2003 (updated)
```

24-JUL-1997 (revised)

25-JAN-1980 (first entry)

DT

DT

```
XX
DE
     Pre-transforming growth factor beta 1 cDNA.
XX
KW
     transforming growth factor beta 1; wound healing;
KW
     recombinant production; ss.
XX
OS
     Homo sapiens.
XX
FH
     Key
                     Location/Qualifiers
FT
     5'UTR
                     1..841
FT
                     /*taq=a
FT
     misc_feature
                     37..113
FT
                     /*tag=b
FT
                      /note= "GC-rich region forms stable hairpin loops;
FT
                              similar to structural organisation of c-myc RNA,
                              could play role in mRNA stability or in
FT
FT
                              regulation of transcription"
FT
     CDS
                      842..2014
FT
                      /*tag= c
                      /product= pre-TGF_beta_1
FT
                      1676..2011
FT
     mat peptide
FΤ
                      /*tag= d
FT
                      /product= mature TGF beta 1
FT
     repeat_region
                      2015..2100
FT
                      /*tag= e
                      /note= "GC-rich region; possibly responsible for the
FT
FT
                              fact 3'UTR of mRNA could not be cloned as cDNA;
                              may be important for transcription efficiency"
FT
                      2019..2023
FT
     repeat_unit
FT
                      /*tag= f
                      2094..2100
FT
     TATA signal
FT
                      /*tag= g
                      /note= "TATA-like sequence; no evidence that this
FT
                              functions a promoter"
FT
FT
     polyA_signal
                      2514..2520
FT
                      /*tag= h
                      2529..2536
FT
     misc_signal
FT
                      /*taq= i
                      /note= "consensus sequence immediately precedes
FΤ
                              polyA-tail (Benoist et al)"
FT
XX
     US5482851-A.
PN
XX
PD
     09-JAN-1996.
XX
PF
     05-NOV-1993;
                    93US-0147364.
XX
                     87US-0025423.
PR
     13-MAR-1987;
PR
     22-MAR-1985;
                     85US-0715142.
     04-AUG-1989;
                     89US-0389929.
PR
     04-MAR-1992;
                     92US-0845893.
PR
                    93US-0147364.
     05-NOV-1993;
PR
XX
PΑ
     (GETH ) GENENTECH INC.
XX
     Derynck RMA, Goeddel DV;
PΙ
XX
```

```
DR
   WPI; 1996-076891/08.
   P-PSDB; AAR90827.
DR
XX
PT
   New recombinant human transforming growth factor-beta prods. - produced
РΤ
   using Chinese hamster ovary cells, for use in diagnostic applications
РΤ
   or in therapy
ХX
PS
   Example 3; Fig 1; 26pp; English.
XX
CC
   The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC
   The nucleotide sequence was obtd. by an analysis of several overlapping
CC
   cDNAs and gene fragments. The DNA is useful for the recombinant
CC
   production of TGF beta 1, which can be used in, e.g. wound healing.
CC
   (Revised entry submitted to correct sequence analysis breakdown.)
CC
   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
   Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Ouery Match
                   79.9%; Score 956.6; DB 17; Length 2537;
 Best Local Similarity
                   88.5%; Pred. No. 3.5e-193;
 Matches 1059; Conservative
                        0: Mismatches 114: Indels
                                                24; Gaps
                                                          1:
         Qу
          Db
       61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          902 CTGACGCCTGGCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          1082 TACAACAGCACCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141
Db
Ov
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
          1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
       361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
          1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          1322 AAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
Db
```

```
541 TACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
          Db
      1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
QУ
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          Db
      1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1561
       721 TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           Db
      1562 ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
       781 ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
QУ
          1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
       841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
QУ
       901 TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
          1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          Db
      1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
Qу
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
          1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 10
ABQ76674
   ABQ76674 standard; DNA; 2527 BP.
ID
XX
AC
   ABQ76674;
XX
DT
   26-MAR-2003 (first entry)
XX
DE
   Androgen receptor signalling pathway-associated DNA E00973.
XX
```

Androgen receptor; transactivation; modulator; Smad3; Smad4; Akt; TGF-B;

KW

```
KW
    signal transduction pathway; transforming growth factor-B; phosphatase;
KW
    tensin; cytostatic; antiproliferative; cellular proliferation; cancer;
KW
    E00973; ds.
XX
OS
    Synthetic.
XX
ΡN
    WO200282081-A2.
XX
ÞΠ
    17-OCT-2002.
XX
PF
    05-APR-2002; 2002WO-US11086.
XX
PR
    06-APR-2001; 2001US-282266P.
    13-MAR-2002; 2002US-365060P.
PR
XX
PA
    (UYRP ) UNIV ROCHESTER.
XX
PΙ
    Chang C;
XX
DR
    WPI; 2003-046871/04.
XX
PΤ
    Modulating androgen receptor activity, by administering a compound that
РΤ
    modulates receptor activity, inhibits receptor-signal transduction
РΤ
    pathway/receptor-coactivator interaction or changes amount or receptor
PΤ
XX
PS
    Disclosure; Page 225-226; 302pp; English.
XX
CC
    This invention describes a novel method for modulating androgen receptor
CC
    activity or androgen receptor-mediated transactivation activity in a
CC
    cell. The method involves administering a compound which causes
CC
    modulation of the androgen receptors activity and the inhibition of
CC
    interaction between the receptor and a protein involved in a signal
CC
    transduction pathway. The compound also inhibits the interaction between
CC
    the androgen receptor and a protein selected from Smad3, Smad4, Akt,
CC
    transforming growth factor (TGF)-B and phosphatase and tensin homologues
CC
    deleted on chromosome 10 (PTEN) or their fragments. The compounds of the
CC
    invention have cytostatic and antiproliferative activity. The obtained
CC
    composition is useful for treating any disease, where uncontrolled
CC
    proliferation or cellular proliferation occurs such as cancer, e.g.
CC
    prostate cancer. This sequence represents the androgen receptor
CC
    transactivation signalling pathway modulator E00973 described in
CC
    the method of the invention.
XX
SO
    Sequence 2527 BP; 472 A; 888 C; 735 G; 432 T; 0 other;
 Query Match
                       79.8%; Score 955; DB 25; Length 2527;
 Best Local Similarity
                       88.4%; Pred. No. 7.6e-193;
 Matches 1058; Conservative
                            0; Mismatches 115; Indels
                                                         24; Gaps
                                                                     1;
          Qу
            Db
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            Dh
         902 CTGACGCCTGGCCCGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
```

Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	962	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	1021
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGAGGTGCCGCCCGGCCCGAGGCCGTGCTCGCCCTC	1081
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	1141
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC	1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777

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961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
            1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
            1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
            1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Oy
            1958 AAGCCCAAGGTGGAGGAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Dh
RESULT 11
AAQ56923
ID
    AAQ56923 standard; cDNA; 2537 BP.
XX
AC
    AAQ56923;
XX
DT
    25-MAR-2003 (updated)
    09-JUL-1994 (first entry)
DT
XX
    Human pre-TGF-beta-1.
DE
XX
    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW
    transforming growth factor beta-3; recombinant; wound healing;
KW
KW
    vulnerary; ss.
XX
    Homo sapiens.
OS
XX
                  Location/Qualifiers
FH
    Key
    misc structure 47..113
FT
                  /*tag= a
FT
                  /note= "possible hairpin loop region"
FT
                  842..2014
FT
    CDS
                  /*tag=b
FT
                  1676..2011
FT
    mat peptide
FT
                  /*tag= c
                  2515..2521
FT
    polyA signal
FT
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XX
PN
    US5284763-A.
XX
PD
    08-FEB-1994.
XX
    04-MAR-1992;
                 92US-0845893.
PF
XX
PR
    22-MAR-1985;
                 85US-0715142.
PR
    13-MAR-1987;
                 87US-0025423.
                 89US-0389929.
PR
    04-AUG-1989;
    04-MAR-1992;
                 92US-0845893.
PR
XX
PA
    (GETH ) GENENTECH INC.
```

```
XX
   Derynk RMA, Goeddel DV;
ΡI
XX
DR
   WPI: 1994-056343/07.
DR
    P-PSDB; AAR46227.
ХX
   Nucleic acid sequences encoding transforming growth factor-beta -
РΤ
    diagnostic probes, and for use in therapeutics
PT
XX
PS
   Disclosure; Fig 1b; 25pp; English.
XX
CC
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
   pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
    respectively). A genomic fragment corresponding to a human TGF-
CC
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
CC
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
    Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
SO
 Query Match
                    79.8%; Score 955; DB 15; Length 2537;
 Best Local Similarity
                    88.4%; Pred. No. 7.7e-193;
                        0; Mismatches 115; Indels
 Matches 1058; Conservative
                                                    Gaps
                                                           1;
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           902 CTGACGCCTGGCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Oy
           1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           Db
       1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACGGGAGCCCGAGCCTGAG 1141
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
           1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
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1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          Db
      1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
          Db
      1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
Db
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACTGCAAGTGGACATCAACGGGTTCACT 1561
Db
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           1562 ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
Db
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
       841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
          1718 TGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
      1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
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RESULT 12
AAN81084
ID AAN81084 standard; cDNA; 1560 BP.
XX
AC AAN81084;
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DT
    25-MAR-2003 (updated)
DT
    09-OCT-1990 (first entry)
XX
DE
    Coding sequence of simian transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS
    Cercopithecus aethiops.
XX
FH
    Key
                  Location/Qualifiers
FT
    CDS
                  261..1433
FT
                  /*taq=a
FT
    sig_peptide
                  282..323
FT
                  /*tag= b
FT
    mat peptide
                  1095..1433
FT
                  /*tag= c
XX
PN
    EP293785-A.
XX
PD
    07-DEC-1988.
XX
ΡF
                 88EP-0108528.
    27-MAY-1988;
XX
PR
    29-MAY-1987;
                 87US-0055662.
                 88US-0147842.
PR
    25-JAN-1988;
XX
    (ONCO ) ONCOGEN.
PA
    (BRIM ) BRISTOL-MYERS CO.
PΑ
XX
    Purchio AG, Gentry L, Twardzik D;
PΙ
XX
    WPI; 1988-347488/49.
DR
    P-PSDB; AAP80647.
DR
XX
    Prodn. of simian transforming growth factor beta-1 - by culturing
PT
    transfected eucaryotic cells, and new precursor proteins, useful for
PT
PT
    treating tumours.
XX
    Disclosure; Page ?; pp; English.
PS
XX
    The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC
    expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC
    between mature simian and human TGF-beta 1. The plasmid also contains
CC
    the SV40 promoter and a selection marker, esp. DHFR.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
CC
CC
    (Updated on 25-MAR-2003 to correct PI field.)
XX
SO
    Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                       79.6%; Score 953.4; DB 9; Length 1560;
 Query Match
                       88.3%; Pred. No. 1.6e-192;
 Best Local Similarity
 Matches 1057; Conservative 0; Mismatches 116; Indels
                                                         24; Gaps
           Qу
            Db
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Qy	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	321	CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG	380
Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	381	GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGCCCGCCCGAGGCCGTGCTCGCCCTG	500
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGGGGGGGGG	560
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	561	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	621	TATGACAAGTTCAAGCAGAGCACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	681		740
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	741	AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	800
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	860
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	861	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	920
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	921	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	981	ACCGGCCGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1040
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1041	ATGGCCACCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	1094
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1095		1136
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960

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1137 TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1196
Db
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
QУ
            1197 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1256
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
QУ
            1257 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1316
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
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Dh
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1377 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
Dh
RESULT 13
AA003508
    AAQ03508 standard; DNA; 1560 BP.
XX
AC
    AAQ03508;
XX
    25-MAR-2003 (updated)
DT
    09-JAN-2003 (updated)
DT
    14-AUG-1990 (first entry)
DT
XX
DE
    Simian Transforming growth factor - Betal.
XX
    HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW
    factors; ds.
KW
XX
    Cebus apella.
OS
XX
FΗ
                 Location/Qualifiers
    Key
                 267..1437
FT
    CDS
FT
                  /*taq=a
                 1103..1437
FT
    mat peptide
FT
                  /*tag=b
XX
PN
    EP356935-A.
ХX
PD
    07-MAR-1990.
XX
PF
    25-AUG-1989; 89EP-0115719.
XX
    25-AUG-1988; 88US-0236698.
PR
XX
    (ONCO ) ONCOGEN LP.
PΑ
XX
    Brankovan V, Lioubin M, Purchio A;
PΙ
XX
    WPI; 1990-068723/10.
DR
    P-PSDB; AAR05663.
DR
```

```
XX
PT
   Compsns. contq. transforming growth factor beta -
PT
   used for inhibitions of HIV infection and replication in vivo.
XX
PS
   Disclosure; Fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in vivo to prevent formation of synctia and
   inhibit HIV infection. TGF may also be used with other HIV treatments
CC
CC
   (AZT, soluble CD4 etc.).
   (Updated on 09-JAN-2003 to add missing OS field.)
CC
   (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
 Query Match
                   79.6%; Score 953.4; DB 11; Length 1560;
 Best Local Similarity 88.3%; Pred. No. 1.6e-192;
                        0; Mismatches 116; Indels
 Matches 1057; Conservative
                                                24; Gaps
                                                          1;
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Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          321 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG 380
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          381 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 440
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qy
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Db
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Qу
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Db
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Db
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Db
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Qу
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Db
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Qу
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Db
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Qу
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Db
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Qу
           Db
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Qу
          Db
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Qу
                        Db
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       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
QУ
          1137 TGCTGCGTGCGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1196
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1197 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1256
Db
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
          1257 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1316
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          1317 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1376
Db
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QУ
          1377 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
Db
RESULT 14
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ID
XX
AC
   AAV52933;
XX
DT
   25-MAR-2003
             (updated)
DT
   21-DEC-1998
             (first entry)
XX
   Human pre-transforming growth factor-beta 1 cDNA.
DΕ
XX
   Transforming growth factor-beta 1; TGF-beta 1; human; ss.
KW
XX
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OS

XX

Homo sapiens.

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FT
     mat peptide
                     1676..2011
FT
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FT
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FT
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FT
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FT
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                     /note= "GC-rich sequence"
FT
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                     2514..2520
FT
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XX
PN
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XX
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XX
PF
     30-MAY-1995;
                    95US-0454468.
XX
PR
     13-MAR-1987;
                    87US-0025423.
PR
     22-MAR-1985;
                    85US-0715142.
PR
     04-AUG-1989;
                    89US-0389929.
PR
     04-MAR-1992;
                   92US-0845893.
PR
     05-NOV-1993;
                   93US-0147364.
     30-MAY-1995;
                    95US-0454468.
PR
XX
PA
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA, Goeddel DV;
XX
     WPI; 1998-494840/42.
DR
     P-PSDB; AAW78785.
DR
XX
PT
     DNA encoding transforming growth factor-beta precursor sequence -
PT
     useful for analysis to perform manipulations to increase yield of
PT
     recombinant production of the protein
XX
     Example 3; Fig 1B 1-3; 26pp; English.
PS
XX
CC
     This nucleotide sequence codes for the human transforming growth
     factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC
CC
     composite of overlapping cDNA clones isolated from different cDNA
     libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC
     TGF-beta exon (see AAV52936) restriction fragments as probes.
CC
     The 3' region of the sequence was determined using cloned genomic
CC
CC
          The invention relates to the recombinant production of
CC
     TGF-beta. Biologically active TGF-beta is defined as being capable
CC
     of inducing EGF-potentiated anchorage independent growth of target
CC
     cell lines and/or growth inhibition of neoplastic cell lines.
CC
     Nucleic acids encoding TGF-beta have been isolated and cloned into
CC
     vectors which are replicated in bacteria and expressed in
CC
     eukaryotic cells. TGF-beta recovered from transformed cells is
CC
     used in known therapeutic applications. TGF-beta nucleic acids are
CC
     also useful in diagnosis and identification of TGF-beta clones.
CC
     (Updated on 25-MAR-2003 to correct PF field.)
XX
```

Location/Qualifiers

FΗ

Key

79.5%; Score 951.8; DB 19; Length 2537; Query Match 88.2%; Pred. No. 3.6e-192; Best Local Similarity Matches 1056: Conservative 0; Mismatches 117; Indels 24; Gaps 1; Qу Db 61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120 Qу Db 902 CTGACGCCTGGCCCGCCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCAG 961 121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180 Qу 962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021 Db 181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240 Qy 1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081 Db 241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300 Qу 1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141 Db 301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360 Qу 1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201 Db 361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420 Qу 1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261 Db 421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480 Qу 1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321 Db 481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540 Qу 1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381 Db 541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600 Qу 1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441 Db 601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660 Qу 1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGAGAAATTGAGGGCTTTCGCCTTAGC 1501 Db 661 GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720 Qу 1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1561 Db 721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780 Qу 1562 ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621 Db

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781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
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Db
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Qу
                          -GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
           1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           Db
       1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
           1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
           1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
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Qу
           1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 15
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ID
XX
AC
    ABV75391;
XX
DT
    18-MAR-2003 (first entry)
XX
    TGFB1 Arg25Pro polymorphism G-allele nucleotide sequence.
DΕ
XX
    Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
KW
    renal failure; nephrotropic; human; gene; ds.
KW
XX
OS
    Homo sapiens.
XX
                 Location/Qualifiers
FΗ
    Key
                 1..1176
FT
    CDS
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FT
XX
    WO200290585-A2.
PN
XX
PD
    14-NOV-2002.
XX
    08-MAY-2002; 2002WO-GB02066.
PF
XX
    09-MAY-2001; 2001GB-0011277.
PR
XX
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```
(UYSH-) UNIV SHEFFIELD HALLAM.
PΑ
ХX
ΡI
    El-Nahas AM, Blakemore A, Khalil MS;
XX
DR
    WPI; 2003-120560/11.
    P-PSDB; ABB82780.
DR
XX
PΤ
    Determining an individual's susceptibility to the progression of renal
PΤ
    failure comprises detecting the presence of a genetic polymorphism
    pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
PT
    from the individual -
РТ
XX
PS
    Claim 49; Page 58; 62pp; English.
XX
CC
    The invention relates to determining an individual's susceptibility to
CC
    renal failure and invovles detecting the presence of a genetic
CC
    polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
CC
    a sample from an individual, where polymorphism pattern is associated
    with renal failure. The method is useful for determining an individual's
CC
    susceptibility to the progression of renal failure. The nucleic acid
CC
CC
    comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
CC
    comprising a sequence of 391 amino acids is useful for preparing a
CC
    medicament for retarding or preventing the progression of renal disease,
CC
    and for drug research purposes for retarding or preventing the
CC
    progression of renal disease. Sequences ABV75386-88 represents the
    nucleotide sequence for the TGFB1 G-allele of the Arg25Pro polymorphism
CC
CC
    of exon 1.
XX
SO
    Sequence 1176 BP; 239 A; 381 C; 354 G; 202 T; 0 other;
                     79.0%; Score 945.2; DB 25; Length 1176;
                     88.3%; Pred. No. 8.1e-191;
 Best Local Similarity
 Matches 1060; Conservative 0; Mismatches 113; Indels
                                                    27; Gaps
                                                               2;
Qу
          Db
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
QУ
           61 CTGACGCCTGGCCGGCCGCCGCGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 120
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
            121 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 180
Db
        181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
           Db
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Qу
           241 TACAACAGCACCGCGACCGGGTGGCCGGGGAAGCTGCAGACCCGAGCCTGAG 300
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Dh
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Qy	478	CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG	537
Db	481	CTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG	540
Qy	538	CGCTACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	541	CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT	600
Qу	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	601	GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT	660
Qу	658	AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	661	AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC	720
Qy	718	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	721	ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT	780
Qy	778	CTCATGGCCACCCGGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	781	CTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	837
Qy	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Db	838	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAG	876
Qy	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
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Qy	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	101
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Qy	1018	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1077
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Qy	1078	GCGGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	113
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Qу	1138	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA	119
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Job time : 373.617 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27; Search time 355.784 Seconds

(without alignments)

9022.658 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	Result Query						
]	No.	Score	Match	Length	DB	ID	Description
	1	958.2	80.1	1821	14	US-10-087-268-1	Sequence 1, Appli
	2	958.2	80.1	2742	14	US-10-037-270-220	Sequence 220, App
	3	956.6	79.9	1821	14	US-10-087-268-4	Sequence 4, Appli
	4	943.6	78.8	2745	11	US-09-948-002-28	Sequence 28, Appl
	5	854.2	71.4	1585	11	US-09-948-002-27	Sequence 27, Appl
	6	847.8	70.8	2094	11	US-09-948-002-1	Sequence 1, Appli
	7	654	54.6	1376	10	US-09-756-283A-19	Sequence 19, Appl
	8	591.4	49.4	1352	10	US-09-756-283A-21	Sequence 21, Appl
	9	344	28.7	489	11	US-09-911-904-167	Sequence 167, App
	10	308.6	25.8	339	10	US-09-813-271B-1	Sequence 1, Appli
	11	227.2	19.0	336	10	US-09-813-271B-7	Sequence 7, Appli
	12	225.6	18.8	4382	12	US-09-957-458B-9	Sequence 9, Appli
	13	224.4	18.7	2574	11	US-09-906-158-3	Sequence 3, Appli
	14	224.4	18.7	2574	13	US-10-028-158-20	Sequence 20, Appl
	15	220.4	18.4	2879	11	US-09-906-158-10	Sequence 10, Appl
	16	209.4	17.5	339	10	US-09-813-271B-5	Sequence 5, Appli
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	18	182.4	15.2	336	10	US-09-813-271B-11	Sequence 11, Appl
	19	181.2	15.1	2381	12	US-10-311-455-2383	Sequence 2383, Ap
	20	180.8	15.1	336	10	US-09-813-271B-9	Sequence 9, Appli
	21	166.2	13.9	4267	11	US-09-948-002-47	Sequence 47, Appl
	22	158.2	13.2	339	10	US-09-813-271B-3	Sequence 3, Appli
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С	39	64	5.3	363	10	US-09-833-381-585	Sequence 585, App
_	40	62.6	5.2	364	12	US-10-029-386-26476	Sequence 26476, A
	41	62.6	5.2	544	12	US-10-029-386-12776	Sequence 12776, A
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	45	52	4.3	1004	8	US-08-957-425-10	Sequence 10, Appl
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## ALIGNMENTS

RESULT 1 US-10-087-268-1

<sup>;</sup> Sequence 1, Application US/10087268; Publication No. US20030119010A1

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; GENERAL INFORMATION:
  APPLICANT: Jonsonn, Julie Ruth
  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
  FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEO ID NO 1
  LENGTH: 1821
   TYPE: DNA
   ORGANISM: Human
  FEATURE:
  NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (512)..(598)
  OTHER INFORMATION:
  NAME/KEY: 3'UTR
  LOCATION: (1685)..(1821)
  OTHER INFORMATION:
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 Query Match
 Best Local Similarity
                   88.6%; Pred. No. 1.2e-258;
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Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1051
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Db	1052	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1111
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
Db	1112	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1171
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
Db	1172	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1231
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Db	1232	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1291
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
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Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
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Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
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RESULT 2
US-10-037-270-220
; Sequence 220, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
  APPLICANT: Liu, Chenghua
  APPLICANT: Asundi, Vinod
  APPLICANT: Zhang, Jie
  APPLICANT: Ren, Feiyan
  APPLICANT: Chen, Rui-hong
  APPLICANT: Zhao, Qing A.
  APPLICANT: Wehrman, Tom
  APPLICANT: Xue, Aidong J.
  APPLICANT: Yang, Yonghong APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yunqing
  APPLICANT: Wang, Dunrui
  APPLICANT: Wang, Zhiwei
  APPLICANT: Tillinghast, John
  APPLICANT: Drmanac, Radoje T.
  TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
  TITLE OF INVENTION: Polypeptides
  FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/10/037,270
 CURRENT FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 09/552,317
  PRIOR FILING DATE: 2000-04-25
  PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1104
  SOFTWARE: pt FL genes Version 1.0
; SEQ ID NO 220
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  ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (842)..(2014)
US-10-037-270-220
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 Best Local Similarity 88.6%; Pred. No. 1.3e-258;
 Matches 1060; Conservative 0; Mismatches 113; Indels 24; Gaps
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Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
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Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
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Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
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Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
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Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC	1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1778	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1837

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       1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
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; Sequence 4, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
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  ORGANISM: Human
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  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
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Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
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Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
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Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	872	TATGACAAGTTCAAGCAGAGTACACACACAGCATATATAT	931
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	991
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1051
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1052		1111
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1112	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1171
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1172		1231
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1232	ACCGCCGCCGAGGTGACCTGCCCACCATTCATGCCATGAACCGGCCTTTCCTGCTTCTC	1291
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1292	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1345
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1346		1387
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RESULT 4
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; Sequence 28, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                           EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
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  NAME/KEY: CDS
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US-09-948-002-28
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 Best Local Similarity 88.2%; Pred. No. 1.7e-254;
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Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCGGGGGGGGGGGGGGGGGGGGGGGGGGCCGGGGCCTGAG	1141
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGG	477
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Qу	478	CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG	537
Db	1322	CTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG	1381
Qy	538	CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	1382	CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT	1441
Qу	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	1442	GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT	1501
Qу	658	AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	1502	AGCGCCCACTGCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC	1561
Qy	718	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	1562	ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT	1621
Qу	778	CTCATGGCCACCCGGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	1622	CTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCCGCCGA	1678
Qу	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Ūb	1679		1717
Qу	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
Db	1718	AACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATC	1777
Qу	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
Db	1778	CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGC	1837

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1018 CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG 1077
Qу
           1838 CTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCG 1897
Db
       1078 GCGGCGCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC 1137
Qу
           Db
       1898 GCGGCGCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGC 1957
       1138 CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           Db
       1958 CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2017
RESULT 5
US-09-948-002-27
; Sequence 27, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                             EXPRESSION
  FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 27
  LENGTH: 1585
   TYPE: DNA
   ORGANISM: Rattus norvegicus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (413)...(1585)
US-09-948-002-27
 Query Match
                    71.4%; Score 854.2; DB 11; Length 1585;
 Best Local Similarity 83.1%; Pred. No. 1.7e-229;
 Matches 995; Conservative 0; Mismatches 178; Indels 24; Gaps
                                                             1:
         QУ
           Db
        413 ATGCCGCCTCGGGGCTGCGGCTGCTGCCGCTTCTGCTCCCACTCCCGTGGCTTCTAGTG 472
        61 CTGACGCCTGGCCGGCCGCCGCACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
QУ
           473 CTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGGAGCTG 532
Dh
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
           Db
        533 GTGAAACGGAAGCGATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGCTCGCC 592
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
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Db	593		652
QУ	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	653	TACAACAGCACCCGCGACCGGGTGGCAGGCGAGAGCGCTGACCCGGAGCCCGAG	712
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	713	GCGGACTACTACGCCAAAGAAGTCACCCGCGTGCTAATGGTGGACCGCAACAACGCAATC	772
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	773	TATGACAAAACCAAAGACATCACACACAGTATATATATGTTCTTCAATACGTCAGACATT	832
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	833	CGGGAAGCAGTGCCAGAACCCCCATTGCTGTCCCGTGCAGAGCTGCGCCTGCAGAGATTC	892
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	893	AAGTCAACTGTGGAGCAACACGTAGAACTCTACCAGAAATATAGCAACAATTCCTGGCGT	952
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	953	TACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCTTTTGACGTC	1012
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1013	ACTGGAGTTGTCCGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGCTTCAGT	1072
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1073		1132
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1133	CCCAAACGTCGAGGTGACCTGGGCACCATCCATGACATGAACCGACCCTTCCTGCTCCTC	1192
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1193	ATGGCCACCCCCTGGAAAGGGCTCAACACCTGCACAGCTCCAGGCACCGGAGA	1246
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1247		1288
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1289	TGCTGTGTACGGCAGCTGTACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCAC	1348
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1349	GAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGGCCCTGCCCCTACATTTGGAGCCTG	1408
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080

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Db
       Qу
       1081 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
           Db
       1469 TCACCGTGCTGCGCGCAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGC 1528
QУ
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
           Db
       1529 AAGCCCAAGGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1585
RESULT 6
US-09-948-002-1
; Sequence 1, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
 APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                           EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
  LENGTH: 2094
   TYPE: DNA
  ORGANISM: Mus musculus
  FEATURE:
   NAME/KEY: CDS
  LOCATION: (868)...(2040)
US-09-948-002-1
 Query Match
                   70.8%; Score 847.8; DB 11; Length 2094;
 Best Local Similarity 82.8%; Pred. No. 1.2e-227;
 Matches 991; Conservative 0; Mismatches 182; Indels
Qу
         Db
       868 ATGCCGCCTCGGGGCTGCGGCTACTGCCGCTTCTGCTCCCACTCCCGTGGCTTCTAGTG 927
Qу
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
           Db
       928 CTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGGAGCTG 987
Qу
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
           Db
       988 GTGAAACGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGCTCGCC 1047
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          Db
       1048 AGTCCCCCAAGCCAGGGGGAGGTACCGCCCGGCCCGCTGCCCGAGGCGGTGCTCGCTTTG 1107
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Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1108		1167
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1168	GCGGACTACTATGCTAAAGAGGTCACCCGCGTGCTAATGGTGGACCGCAACAACGCCATC	1227
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1228	TATGAGAAAACCAAAGACATCTCACACAGTATATATGTTCTTCAATACGTCAGACATT	1287
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1288	CGGGAAGCAGTGCCCGAACCCCCATTGCTGTCCCGTGCAGAGCTGCGCTTGCAGAGATTA	1347
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1348	AAATCAAGTGTGGAGCAACATGTGGAACTCTACCAGAAATATAGCAACAATTCCTGGCGT	1407
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1408		1467
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1468	ACTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGATTCAGC	1527
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1528	GCTCACTGCTCTTGTGACAGCAAAGATAACAAACTCCACGTGGAAATCAACGGGATCAGC	1587
Qy	721	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1588	CCCAAACGTCGGGGCGACCTGGGCACCATCCATGACATGAACCGGCCCTTCCTGCTCCTC	1647
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1648	ATGGCCACCCCCTGGAAAGGGCCCAGCACCTGCACAGCTCACGGCACCGGAGA	1701
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1702	GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAAC	1743
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1744	TGCTGTGTGCGGCAGCTGTACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCAC	1803
Qу	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1804	GAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTATATTTGGAGCCTG	1863
Qу	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1864	GACACACAGTACAGCAAGGTCCTTGCCCTCTACAACCAAC	1923
Qу	1081	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140

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Db
      1924 TCACCGTGCTGCGCGCAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGC 1983
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
      1984 AAGCCCAAGGTGGAGCAGTTGTCCAACATGATTGTGCGCTCCTGCAAGTGCAGCTGA 2040
RESULT 7
US-09-756-283A-19
; Sequence 19, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
 APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
  LENGTH: 1376
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: LAP-mIFNbeta construct
   NAME/KEY: CDS
   LOCATION: (1)..(1368)
US-09-756-283A-19
 Query Match
                   54.6%; Score 654; DB 10; Length 1376;
 Best Local Similarity
                   88.1%; Pred. No. 2.4e-173;
 Matches 724; Conservative
                       0; Mismatches 95; Indels
                                                 3; Gaps
                                                          1;
         Qу
          Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
QУ
          61 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 120
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
          Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 180
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          Db
       181 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 240
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          241 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGATGCAGAACCGGAGCCCGAGCCTGAG 300
Db
0v
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
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Db
       301 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 360
       361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          Db
       361 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 420
Qу
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT---GAGG 477
          421 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGG 480
Db
       478 CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG 537
Qу
          481 CTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG 540
Db
       538 CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT 597
Qу
          541 CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT 600
Db
       598 GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC 657
Qу
          601 GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT 660
Db
       658 AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC 717
Qу
          Db
       661 AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC 720
       718 AATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC 777
Qу
          721 ACTACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT 780
Dh
       778 CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGC 819
Qу
          Db
       781 CTCATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGC 822
RESULT 8
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## US-09-756-283A-21 ; Sequence 21, Application US/09756283A ; Patent No. US20020151478A1 ; GENERAL INFORMATION: APPLICANT: Chernajovsky, Yuti APPLICANT: Dreja, Hanna Stina APPLICANT: Adams, Gillian TITLE OF INVENTION: Latent Fusion Protein FILE REFERENCE: 0623.1000000 CURRENT APPLICATION NUMBER: US/09/756,283A CURRENT FILING DATE: 2001-01-09 NUMBER OF SEQ ID NOS: 100 SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 21 LENGTH: 1352 TYPE: DNA ORGANISM: Artificial Sequence

OTHER INFORMATION: mIFNbeta-LAP construct

FEATURE:

NAME/KEY: CDS

; LOCATION: (1)..(1344) US-09-756-283A-21

	cal S	49.4%; Score 591.4; DB 10; Length 1352; Similarity 87.0%; Pred. No. 8.6e-156; 2; Conservative 0; Mismatches 96; Indels 3; Gaps	1;
Qу	63	GACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTGGT 1	L22
Db	582		541
Qy	123	GAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAG 1	L82
Db	642	GAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAG 7	701
Qy	183	CCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTA 2	242
Db	702	CCCCCGAGCCAGGGGGGGGGCCGCCCGGCCCGAGGCCGTGCTCGCCCTGTA 7	761
Qy	243	CAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGC 3	302
Db	762		321
Qy	303	GGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTA 3	362
Db	822		381
Qy	363	TGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCG 4	122
Db	882		941
Qy	423	GGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCT 4	179
Db	942		1001
Qy	480	CAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCG 5	539
Db :	1002		1061
Qy	540	CTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGT 5	599
Db :	1062		121
Qy	600	CACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAG 6	559
Db :	1122		181
Qy	660	TGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA 7	719
Db :	1182		241
Qy	720	TTCTGGCCGCCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCT 7	779
Db 3	1242	TACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCT 1	301
Qy	780	CATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCT 820	

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RESULT 9
US-09-911-904-167
; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
 APPLICANT: Farr, Spencer B.
 APPLICANT: Pickett, Gavin G.
 APPLICANT: Neft, Robin Eileen
 APPLICANT: Dunn, II, Robert Thomas
  TITLE OF INVENTION: CANINE TOXICITY GENES
  FILE REFERENCE: 400742000200
  CURRENT APPLICATION NUMBER: US/09/911,904
  CURRENT FILING DATE: 2002-04-09
  PRIOR APPLICATION NUMBER: US 60/220,057
 PRIOR FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 386
  SOFTWARE: FastSEO for Windows Version 4.0
; SEO ID NO 167
   LENGTH: 489
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: misc feature
   LOCATION: (1)...(489)
   OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
 Query Match
                     28.7%; Score 344; DB 11; Length 489;
 Best Local Similarity 89.9%; Pred. No. 1.6e-86;
 Matches 390; Conservative 0; Mismatches 20; Indels 24; Gaps
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Qу
           1 GACCCTTCCTGCTCCTCATGGCCACCCCACTGGAGAGGGCCCAGCACCTGCACAGCTCCC 60
Db
        824 GGCACCGCGAGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCA 883
Qу
           Db
         61 GGCAGCGCCG--------GGCCCTGGACACCAACTACTGCTTCA 96
        884 GCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGG 943
Qу
           97 GCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCTCTACATTGACTTCCGCAAGGATCTGG 156
Db
        944 GCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTC 1003
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           Db
        157 GCTGGAAGTGGATCCATGAGCCCAAGGGTTACCACGCTAACTTCTGCCTGGGGCCCTGCC 216
       1004 CCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACA 1063
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           Db
        217 CCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCACA 276
       1064 ACCCGGGCGCGTCGGCGCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCG 1123
Qу
           Db
        277 ACCCGGGCGCGTCGGCGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCG 336
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Qу
        1124 TGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCT 1183
             Db
         337 TGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCGAACATGATCGTGCGCTCCT 396
        1184 GCAAGTGCAGCTGA 1197
Qу
             Db
         397 GCAAGTGCAGCTGA 410
RESULT 10
US-09-813-271B-1
; Sequence 1, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
        APPLICANT:
                    (A) Nico Cerletti
        TITLE OF INVENTION: New process for the production of
                            biologically active protein
        NUMBER OF SEQUENCES: 13
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: No. US20020115834Alartis Patent Department
             STREET: 564 Morris Avenue
             CITY: Summit
             STATE: New Jersey
             COUNTRY: USA
             ZIP: 07901
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/813,271B
             FILING DATE: 20-Mar-2001
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: PCT/EP95/02719
             FILING DATE: 12-Jul-95
             APPLICATION NUMBER: EPO 94810439.3
             FILING DATE: 25-Jul-94
        ATTORNEY/AGENT INFORMATION:
             NAME: Pfeiffer, Hesna J. .
             REGISTRATION NUMBER: 22640
             REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (908) 522-6940
             TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 1:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 339 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA to mRNA
        HYPOTHETICAL: NO
        IMMEDIATE SOURCE:
             CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
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FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "human TGF-betal"
       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1
 Query Match
                    25.8%; Score 308.6; DB 10; Length 339;
 Best Local Similarity
                   94.4%; Pred. No. 1.3e-76;
 Matches 320; Conservative
                         0; Mismatches
                                     19; Indels
                                                 0; Gaps
                                                           0;
Qу
       Db
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RESULT 11
US-09-813-271B-7
; Sequence 7, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
      APPLICANT:
               (A) Nico Cerletti
      TITLE OF INVENTION: New process for the production of
                      biologically active protein
      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834Alartis Patent Department
          STREET: 564 Morris Avenue
          CITY: Summit
          STATE: New Jersey
          COUNTRY: USA
          ZIP: 07901
      COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/813,271B
            FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: PCT/EP95/02719
            FILING DATE: 12-Jul-95
            APPLICATION NUMBER: EPO 94810439.3
            FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
            NAME: Pfeiffer, Hesna J. .
            REGISTRATION NUMBER: 22640
            REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (908) 522-6940
            TELEFAX: (908) 522-6955
  INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 336 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "recombinant hybrid DNA of
       IMMEDIATE SOURCE:
            CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
       FEATURE:
            NAME/KEY: mat peptide
            LOCATION: 1..132
            OTHER INFORMATION: /product= "N-terminal 44 amino
            acids of human TGF-betal"
       FEATURE:
            NAME/KEY: mat peptide
            LOCATION: 133..336
            OTHER INFORMATION: /product = "C-terminal 68 amino
            acids of human TGF-beta3"
       FEATURE:
            NAME/KEY: CDS
            LOCATION: 1..336
            OTHER INFORMATION: /product = "hybrid TGF-beta named
            TGF-beta1-3"
       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-813-271B-7
 Query Match
                      19.0%; Score 227.2; DB 10; Length 336;
 Best Local Similarity 79.8%; Pred. No. 8.6e-54;
 Matches 268; Conservative
                           0; Mismatches
                                         68; Indels 0; Gaps
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        Db
          919 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 978
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            Db
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            Db
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RESULT 12
US-09-957-458B-9
; Sequence 9, Application US/09957458B
; Publication No. US20030166271A1
; GENERAL INFORMATION:
  APPLICANT: Chen, Una
  TITLE OF INVENTION: Method for growing stem cells
 FILE REFERENCE: P66567US0
 CURRENT APPLICATION NUMBER: US/09/957,458B
 CURRENT FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: PCT/EP00/08247
 PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: EP 99116533
 PRIOR FILING DATE: 1999-08-24
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 9
  LENGTH: 4382
  TYPE: DNA
  ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Vector for transforming supporting cell with a foreign to
express
   OTHER INFORMATION: a gene product of interest
US-09-957-458B-9
                     18.8%; Score 225.6; DB 12; Length 4382;
 Query Match
 Best Local Similarity 52.2%; Pred. No. 4.9e-53;
 Matches 652; Conservative 0; Mismatches 524; Indels 72; Gaps
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            575 GTGGAAGCCATTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCA 634
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Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	809	AATGAACTGGCCGTCTGCCCCAAAGGAATTACCTCTAAGGTTTTTCGTTTCAATGTGTCC	868
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	869	TCAGTGGAGAAAATGGAACCAATCTGTTCCGGGCAGAGTTCCGGGTCTTGCGGGTGCCC	928
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAA	519
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Qy	520	TACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCG	579
Db	989	GAGCACATAGCCAAGCAGCGCTACATAGGTGGCAAGAATCTGCCCACAAGGGGCACCGCT	1048
Qy	580	GAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCT	639
Db	1049	GAATGGCTGTCTTTCGATGTCACTGACACTGTGCGCGAGTGGCTGTTGAGGAGAGAGTCC	1108
Qy	640	ATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGC	681
Db	1109	AACTTGGGTCTGGAAATCAGCATCCACTGTCCATGTCACACCTTTCAGCCCAATGGAGAC	1168
Qy	682	AAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGC	729
Db	1169	ATACTGGAAAATGTTCATGAGGTGATGGAAATCAAATTCAAAGGAGTGGACAATGAAGAT	1228
Qy	730	CGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACC	789
Db	1229		1288
Qу	790	CCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGAC	849
Db	1289	CTGATCCTCATGATGATCCCCCCACACCGACTGGACAGCCCAGGCCAGGCCAGGCAGTCAGAGG	1348
Qy	850	GACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTG	909
Db	1349	AAGAAGAGGGCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGTA	1408
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Db	1409	CGCCCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAG	1468

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RESULT 13
US-09-906-158-3
; Sequence 3, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
 FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
 NUMBER OF SEQ ID NOS: 168
SEQ ID NO 3
  LENGTH: 2574
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
   NAME/KEY: CDS
   LOCATION: (254) ... (1492)
US-09-906-158-3
 Query Match
                   18.7%; Score 224.4; DB 11; Length 2574;
 Best Local Similarity 53.3%; Pred. No. 9.2e-53;
 Matches 660; Conservative 0; Mismatches 506; Indels
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Qу	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT	370
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Qу	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG	430
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Db	675	AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT	734
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QУ	590	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT	649
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Qу		AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC	
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Qy -		GGCCCTTCCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGC	
	-	GTGGAGATCTGGGGCGCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA	
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		TGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGTCAGAGGAAGAAGCGGG	
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		CTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTCT	
Qy Dh		ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG	
		ACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTATG	
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RESULT 14
US-10-028-158-20
; Sequence 20, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
  APPLICANT: Caniggia, Isabella
  APPLICANT: Post, Martin
  APPLICANT: Lye, Stephen
  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
  TITLE OF INVENTION: TROPHOBLAST
 FILE REFERENCE: 11757.38USWO
  CURRENT APPLICATION NUMBER: US/10/028,158
  CURRENT FILING DATE: 2001-12-20
  PRIOR APPLICATION NUMBER: US/09/380,662
  PRIOR FILING DATE: 1999-12-21
  PRIOR APPLICATION NUMBER: PCT/CA98/00180
  PRIOR FILING DATE: 1998-03-05
 PRIOR APPLICATION NUMBER: US 60/039,919
 PRIOR FILING DATE: 1997-03-07
 NUMBER OF SEO ID NOS: 24
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
   LENGTH: 2574
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)..(1492)
US-10-028-158-20
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                     18.7%; Score 224.4; DB 13; Length 2574;
 Best Local Similarity 53.3%; Pred. No. 9.2e-53;
 Matches 660; Conservative 0; Mismatches 506; Indels 72; Gaps
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Db	495		554
Qy	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT	370
Db	555	ATGCCAAAGAAATCCATAAATTCGACATGATCCAGGGGCTGGCGGAGCACAACGAACTGG	614
Qу	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG	430
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Qу	431	TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAG	490
Db	675	AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT	734
Qу	491	TGGAGCACGTGGAGCTATACCAGAAATACAGCAATG	529
Db	735	CTAAGCGGAATGAGCAGAGCACCACTCCCAGATCCTTCCGGCCAGATGAGCACATTG	794
Qy	530	ATTCCTGGCGCTACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGT	589
Db	795	CCAAACAGCGCTATATCGGTGGCAAGAATCTGCCCACACGGGGCACTGCCGAGTGGCTGT	854
Qy	590		649
Db	855		914
Qy	650	TTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGG	703
Db	915	TAGAAATCAGCATTCACTGTCCATGTCACACCTTTCAGCCCAATGGAGATATCCTGGAAA	974
Qу	704	AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC	763
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Qy	764	GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGC	819
Db	1035	GTGGAGATCTGGGGCGCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA	1094
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Qу	860	CCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	919
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                                                    11111
       1275 CCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACCCACAGCACGG 1334
Db
       Qу
                         1335 TGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCC 1394
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                          1455 TCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 1492
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RESULT 15
US-09-906-158-10
; Sequence 10, Application US/09906158
: Publication No. US20030078217A1
; GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
  FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 10
   LENGTH: 2879
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (611) ... (1843)
US-09-906-158-10
 Query Match
                    18.4%; Score 220.4; DB 11; Length 2879;
 Best Local Similarity 52.1%; Pred. No. 1.3e-51;
 Matches 645; Conservative 0; Mismatches 521; Indels
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Db
        146 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 205
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Qу	266	CCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACT	310
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Qу	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT	370
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Qy	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG	430
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Qy	431	TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCA	481
Db	1026	AAAATGGAACCAATCTGTTCCGGGCAGAGTTCCGGGTCTTGCGGGTGCCCAACCCCAGCT	1085
Qy	482	AGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATG	529
Db	1086	CCAAGCGCACAGAGCAGAATTGAGCTCTTCCAGATACTTCGACCGGATGAGCACATAG	1145
Qy	530	ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGT	589
Db	1146	CCAAGCAGCGCTACATAGGTGGCAAGAATCTGCCCACAAGGGGCACCGCTGAATGGCTGT	1205
Qу	590	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT	649
Db	1206	CTTTCGATGTCACTGACACTGTGCGCGAGTGGCTGTTGAGGAGAGAGTCCAACTTGGGTC	1265
Qу	650	TTCGCCTCAGTGCCCACTCTTCCTCTGACAGC	681
Db	1266	TGGAAATCAGCATCCACTGTCCATGTCACACCTTTCAGCCCAATGGAGACATACTGGAAA	1325
Qy	682	AAAGATAACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACC	739
Db	1326	ATGTTCATGAGGTGATGGAAATCAAATTCAAAGGAGTGGACAATGAAGATGACCATGGCC	1385
Qy	740	TGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGA	799
Db	1386	GTGGAGACCTGGGGCGTCTCAAGAAGCAAAAGGATCACCACACCCACACCTGATCCTCA	1445
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Search completed: October 28, 2003, 09:04:07

Job time : 362.927 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 2970.42 Seconds

(without alignments)

9794.056 Million cell updates/sec

Title: US-10-017-372E-8

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em\_estmu:\*
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7: em\_estro:\*
8: em\_htc:\*
9: gb\_est1:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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VERSION
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            NIH-MGC http://mgc.nci.nih.gov/.
  AUTHORS
  TITLE
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
  JOURNAL
            Contact: Robert Strausberg, Ph.D.
COMMENT
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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            http://image.llnl.gov
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Qу

Db

Qу

Dh

Qу

Db

Qу

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more information about this cluster, see
          http://www.genoscope.cns.fr/
         cgi-bin/cluster.cgi?seq=CS0DI002CE03NP1&cluster=9160.r. Contact :
         Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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ΝĎ
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Qу
           564 AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCGGGGTGACCTGGCCACC 505
Db
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Qу
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504 ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCGGTGGAGAGGGCCCAG 445

Db

&cluster=9160.r. Contact : Feng Liang Email : fliang@lifetech.com

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Qу
       808 CACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGGAT 867
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       Qу
       Db
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       928 TTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTC 987
           Db
       348 TTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTC 289
       988 TGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCT 1047
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           Db
       288 TGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTAMMMCAAGGTCCTGGCC 229
       1048 CTGTACAACCAGCACAACCCGGGCGCGTCGGCGCGCGTGCTGCGTGCCGCAGGCGCTG 1107
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           Db
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      1108 GAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 1167
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           Db
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Qу
           Db
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RESULT 4
BX349319
LOCUS
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                                                 EST 05-MAY-2003
DEFINITION BX349319 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
         Homo sapiens cDNA clone CS0DL010YL07 5-PRIME, mRNA sequence.
ACCESSION
         BX349319
         BX349319.1 GI:30379410
VERSION
KEYWORDS
         EST.
SOURCE
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 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
         1 (bases 1 to 900)
 AUTHORS
         Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
         Full-length cDNA libraries and normalization
 JOURNAL
         Unpublished
COMMENT
         Contact: Genoscope
         Genoscope - Centre National de Sequencage
         BP 191 91006 EVRY cedex - France
         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
         Library was constructed by Life Technologies, a division of
         Invitrogen. This sequence belongs to sequence cluster 9160.r For
         more information about this cluster, see
         http://www.genoscope.cns.fr/
         cgi-bin/cluster.cgi?seq=CS0BAG059ZD04 CS05596_1&cluster=9160.r.
         Contact : Feng Liang Email : fliang@lifetech.com URL :
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

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Faraday Avenue Genoscope sequence ID: CS0BAG059ZD04 CS05596 1.
FEATURES
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               /clone="CSODL010YL07"
               /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
               /cell line="RAMOS CELL LINE"
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               25-NORMALIZED"
               /note="1st strand cDNA was primed with a NotI-oligo(dT)
               primer. Five prime end enriched, double-strand cDNA was
               digested with Not I and cloned into the Not I and EcoR V
               sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
           179 a
                  292 c
                        270 q
                              155 t
                                      4 others
ORIGIN
 Query Match
                  57.0%; Score 682.4; DB 13; Length 900;
 Best Local Similarity 88.4%; Pred. No. 6.4e-145;
 Matches 740; Conservative 0; Mismatches
                                   97;
                                              0;
                                                 Gaps
                                       Indels
                                                       0;
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Qу
          95 CTGACGCCTGGCCGGCCGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 154
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
          155 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 214
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          215 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 274
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
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Db
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          Db
       395 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 454
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Qу
          455 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 514
Db
       481 AAGTTAAAAGTGGAGCACCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
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             Db
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        781 ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC 837
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LOCUS
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                               1041 bp
                                         mRNA
                                                linear
                                                       EST 02-MAY-2003
DEFINITION BX324511 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
          cDNA clone CS0DC024YD20 3-PRIME, mRNA sequence.
ACCESSION
          BX324511
VERSION
          BX324511.1 GI:30332381
KEYWORDS
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SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 1041)
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 AUTHORS
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0AC024DB10NP2&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CSOACO24DB10NP2.
FEATURES
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/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 176 a 283 c 346 g 219 t 17 others ORIGIN

	ocal :	52.6%; Score 629.6; DB 13; Length 1041; Similarity 84.7%; Pred. No. 7.1e-133; 8; Conservative 8; Mismatches 102; Indels 32; Gaps	7;
Qy	269	GGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCC	328
Db	1022	:     :	966
Qу	329	GCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCACA	388
Db	965	GCGTGYTAATGKT-GAAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACACACA	907
Qу	389	GCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGC	448
Db	906	GCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGC	847
Qy	449	TCTCTC-GGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGGAG	507
Db	846	TCTCCCSGGGCAGAGCTGCGTCTGAGGCTCAAGTTAAAAGTGGAGCACGTGGAG	787
Qy	508	CTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCC	567
Db	786	CTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCAGCAACCGGCTGCTGGCACCC	727
Qy	568	AGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACC	627
Db	726	AGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGC	667
Qy	628	CGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGAT	687
Db	666	CGTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGAT	608
Qy	688	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC	747
Db	607	AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCACC	548
Qy	748	ATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAG	807
Db	547	ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCCAG	488
Qy		CACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGGAT	
Db	487	CATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC	452
Qy	868	ACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	927
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        988 TGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCT 1047
            Db
        331 TGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCC 272
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            Db
        271 CTGTACAACCAGCATAACCC-GGCGCCCTCGGCGCGCGCGTG-TGCGTGCCGCAGGCGCTG 214
Qу
        1108 GAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 1167
            213 GAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 154
Db
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        1168 ATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
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DEFINITION AGENCOURT 6544437 NIH MGC_88 Homo sapiens cDNA clone IMAGE:5550039
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ACCESSION
VERSION
          BM555996.1 GI:18796907
KEYWORDS
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SOURCE
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
          1 (bases 1 to 1043)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12261 row: i column: 16
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# Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

BASE COUNT 202 a 329 c 345 g 154 t 13 others ORIGIN

Best Lo	cal .	52.6%; Score 629.4; DB 12; Length 1043; Similarity 88.1%; Pred. No. 7.9e-133; 6; Conservative 0; Mismatches 71; Indels 24; Gaps	1;
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Db	61	TGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGG	120
Qy	506	AGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCC	565
Db	121	AGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCAGCAACCGGCTGCTGGCAC	180
Qy	566	CCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGA	625
Db	181	CCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGA	240
Qу	626	CCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAG	685
Db	241	GCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGG	300
Qу	686	ATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCA	745
Db	301	ATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCA	360
Qу	746	CCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCC	805
Db	361	CCATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCC	420
Qу		AGCACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGG	
Db	421	AGCATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGG	456
Qу	866	ATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	925
Db	457	ACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	516
Qу	926	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATT	985
Db	517	ACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACT	576
Qу	986	TCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGG	1045
Db	577	TCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGG	636
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Db
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LOCUS
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                                                              EST 08-MAY-2003
DEFINITION BX383773 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
           cDNA clone CS0DK001YA15 3-PRIME, mRNA sequence.
ACCESSION
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           BX383773.1 GI:30457168
VERSION
KEYWORDS
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SOURCE
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 ORGANISM Homo sapiens
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
           1 (bases 1 to 950)
 AUTHORS
           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
           Full-length cDNA libraries and normalization
  JOURNAL
           Unpublished
COMMENT
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. This sequence belongs to sequence cluster 9160.r For
           more information about this cluster, see
           http://www.genoscope.cns.fr/
           cgi-bin/cluster.cgi?seq=CS0DK001AA08NP1&cluster=9160.r. Contact :
           Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CSODKOO1AA08NP1.
FEATURES
                    Location/Qualifiers
                    1. .950
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                    sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
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                        260 c
                                 312 g
                                         195 t
                                                   12 others
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                         50.4%; Score 603.6; DB 13; Length 950;
 Best Local Similarity
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Matches	717	7;	Conservative	8;	Mismatche	s 104;	Indels	26;	Gaps	3;
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Qy	403		CAACACGTCGGAGCTC							462
Db	883		CAAMACATCAGAGCTC							824
Qy	463		GCGCCTGCTGAGGCTC							522
Db	823		GCGTCTGCTGAGGCTC							764
Qy	523	AG 	CAATGATTCCTGGCGC	TACC	TCAGCAACCG	GCTGCTGG	CCCCCAGTO	ACTCA	CCGGAG	582
Db	763		CAACAATAMCTGGCGA							704
Qy	583	TG	GCTGTCCTTTGATGTC					GAGAG	GCTATA	642
Db	703	TG	GTTATCTTTTGATGTC					111 1	GAAATT	644
Qy	643	GA	GGGTTTTCGCCTCAGT	rgccc.		rgacagca 		CACTC	CACGTG	702
Db	643	ĠĀ	-GGCTTTCGCCTTAGC						CAAGTG	585
Qу	703		AATTAACGGGTTCAAT		GCCGCCGGGG					762
Db	584		CATCAACGGGTTTACT						, , , , , ,	525
Qy	763	CG(	GCCCTTCCTGCTCCTC		CCACCCCGCTC					822
Db	524	ĊĠ	ĠĊĊŦŦŦĊĊŦĠĊŦŦĊŦĊ							465
Qy		1.1	GCACCGCCGAGACTAC 			11.1		1311	11111	-
Db	464	CG	GCACCGCCGA			GCMC	TGGACACCA	ACTAT	TGCTTC	429
Qy	883	AG	CTCCACGGAGAAGAAC	TGCT	GCGTGCGGCA(	GCTCTACA	TTGACTTCC	GGAAG	GACCTG	942
Db	428	AG	CTCCACGGAGAAGAAC	CTĠĊŦ	GCGTGCGGCA	GCTGTACA	TTKACTTCC	GCAAG	GACCTC	369
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Qy :			CTACATCTGGAGCCTA 	1111				1	1	
du	308	CC	CTACATTTGGAGCCTG	GACA(	CGCAGTACAG	CAAGGTCC	TGGCGCCTG	TACAA	CCAGCA	249
Qy 1			CCGGGCGCGTCGGCG 				111111111	1 111		
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DEFINITION
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ACCESSION
            BX434425
VERSION
            BX434425.1 GI:30779291
KEYWORDS
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SOURCE
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REFERENCE
              (bases 1 to 888)
  AUTHORS
           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  TITLE
            Full-length cDNA libraries and normalization
  JOURNAL
            Unpublished
COMMENT
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 9160.r For
            more information about this cluster, see
           http://www.genoscope.cns.fr/
            cqi-bin/cluster.cqi?seq=CS0BAK028AB08NM1&cluster=9160.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAK028AB08NM1.
FEATURES
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                    Library was not normalized."
BASE COUNT
               156 a
                         253 c
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                                          176 t
                                                     1 others
ORIGIN
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  Best Local Similarity
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  Matches 679; Conservative
                               0; Mismatches
                                                76; Indels
                                                               25;
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Qу
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                     Db
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Qy	538	CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	769	CGATACCTCAGCAACCGGCTGCTGGCACACAGCGACTCGCCAGAGTGGTTATCTTTTGAT	710
Qy	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	709	GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT	650
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Qу	778	CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	529	CTCATGGCCACCCGGTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	473
Qy	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Db	472		434
Qу	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
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Qy	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
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Qу	1018	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1077
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Qу	1078	GCGGCGCGTGCTGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	1137
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RESULT 9 AL530081

LOCUS AL530081 859 bp mRNA linear EST 23-MAY-2003
DEFINITION AL530081 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD009YM06 5-PRIME, mRNA sequence.

ACCESSION AL530081

VERSION AL530081.2 GI:31067916

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          Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 859)
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
 TITLE
 JOURNAL
          Unpublished
COMMENT
          On Feb 13, 2001 this sequence version replaced gi:12793574.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cqi-bin/cluster.cqi?seq=CS0DD009BG03QP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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BASE COUNT
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                             257 g
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 Best Local Similarity
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 Matches 641; Conservative
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KEYWORDS

EST.

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Db		T 725
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Db		
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VERSION	BE312000.1 GI:9130128	
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REFERENCE		
AUTHORS TITLE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC	'\
JOURNAL		. 1
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-r@mail.nih.gov	
	Tissue Procurement: ATCC	

cDNA Library Preparation: Ling Hong/Rubin Laboratory

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          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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                 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
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                 cloned into EcoRI/XhoI sites using the following 5'
                 adaptor: GGCACGAG(G). Library constructed by Ling Hong
                 in the laboratory of Gerald M. Rubin (University of
                 California, Berkeley) using ZAP-cDNA synthesis kit
                 (Stratagene) and Superscript II RT (Life Technologies).
                 Note: this is a NIH MGC Library."
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                     87.4%; Pred. No. 3.9e-119;
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VERSION
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REFERENCE
             (bases 1 to 717)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
          Contact: Robert Strausberg, Ph.D.
COMMENT
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

BASE COUNT 158 a 226 c 213 g 120 t ORIGIN

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ACCESSION
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VERSION
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REFERENCE
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           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
           National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
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                    following 5' adaptor: GGCACGAG(G). Library constructed
                    by Ling Hong in the laboratory of Gerald M. Rubin
                    (University of California, Berkeley) using ZAP-cDNA
                    synthesis kit (Stratagene) and Superscript II RT (Life
                    Technologies). Note: this is a NIH MGC Library."
BASE COUNT
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 Best Local Similarity
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Qy	506		GCTATACCAGAAATAC 							565
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
          1 (bases 1 to 925)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
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                  pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                  source anonymous pool of 6 male brains, age range 23-27; 1
                  male lung, age 27; and 1 male testis, age 69. Library is
                  oligo-dT primed and directionally cloned (EcoRV site is
                  destroyed upon cloning). Average insert size 1.8 kb,
                  insert size range 1-3 kb. Library is normalized and
                  enriched for full-length clones and was constructed by C.
                  Gruber (Invitrogen). Research Genetics tracking code
                  021. Note: this is a NIH MGC Library."
BASE COUNT
              170 a
                      316 c
                              278 g
                                      161 t
ORIGIN
 Query Match
                       44.6%; Score 534.2; DB 12; Length 925;
 Best Local Similarity 87.6%; Pred. No. 3.5e-111;
 Matches 607; Conservative 0; Mismatches 83; Indels
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                                                                    2;
Qу
          ďŪ
         151 ATGCCGCCTCCGGGCTGCGGCTGCTGCTGCTACCGCTGCTGTGGCTACTGGTG 210
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            Db
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         121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
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VERSION

Qy		PAGGGGGACGTGCCGCCCGCCCGCTGCCTGAGGCAGTACTGGCTCTT 2	
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Qу		CGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 3	
Db		CGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	
QУ		CCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 3	360
Db		CCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	510
Qy	361 TATGATAAATTCA 	AGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 4	120
Db		AGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 5	570
Qy		CGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 4	180
Db			530
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Db			590
Qу		GGCTGC-TGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGT 5	599
Db			750
Qy		CGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC 6	557
Db			310
Qy		CCTCTGACAGCAAAGATAAC 690	
Db		CCTGTGACAGCAGGGATACC 843	
RESULT 14 BQ054305			
LOCUS DEFINITION	BQ054305 AGENCOURT 68304	1093 bp mRNA linear EST 29-MAR-2 09 NIH MGC_106 Homo sapiens cDNA clone IMAGE:5936	
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	5', mRNA sequent BQ054305 BQ054305.1 GI: EST. Homo sapiens (he	ce	
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Mammalia; Euther 1 (bases 1 to NIH-MGC http://m National Institut Unpublished Contact: Robert Email: cgapbs-ro	mgc.nci.nih.gov/. utes of Health, Mammalian Gene Collection (MGC)  Strausberg, Ph.D.	. <b>;</b>

```
cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2125 row: k column: 22
          High quality sequence stop: 605.
FEATURES
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                  1. .1093
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                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="IMAGE:5936397"
                  /tissue type="natural killer cells, cell line"
                  /lab host="DH10B (phage-resistant)"
                  /clone lib="NIH MGC 106"
                  /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGCACGAG(G). Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH MGC Library."
BASE COUNT
                     347 c
                                     203 t
             233 a
                             309 g
                                              1 others
ORIGIN
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 Query Match
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        765 GUUCTTCCTGCTCCTCATGGCCACCCGGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCG 824
ÛУ
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Qу
            111111111
                                         Db
        301 GCACCGCCGA-----
                                    -----GCCCTGGACACCAACTATTGCTTCAG 336
Qу
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```
Db
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Db
Qу
        Db
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       1125 GTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTG 1184
Qу
            Db
        577 GTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTG 636
Qу
        1185 CAAGTGCAGCTG 1196
            111111111
Db
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RESULT 15
AL530080/c
LOCUS
          AL530080
                                841 bp
                                         mRNA
                                                linear
                                                        EST 23-MAY-2003
DEFINITION AL530080 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
          cDNA clone CS0DD009YM06 3-PRIME, mRNA sequence.
ACCESSION
          AL530080
VERSION
          AL530080.2 GI:31067915
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
          1 (bases 1 to 841)
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          On Feb 13, 2001 this sequence version replaced gi:12793573.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DD009BG03NP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DD009BG03NP1.
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                /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
            150 a
                   240 c
                          283 g
                                153 t
                                        15 others
ORIGIN
 Query Match
                   43.5%;
                         Score 520.2; DB 9; Length 841;
 Best Local Similarity
                   84.0%; Pred. No. 5.3e-108;
 Matches 647; Conservative
                         7; Mismatches
                                     86;
                                         Indels
                                                30; Gaps
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       841 CGGTACCTGMACCCTTGTTGYTCTCCCCGGGCAGAGCTGCTTCTGCTAAGGCTCAAGTTA 782
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Qу
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Db
       547 AGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGA 606
Qу
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Db
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Qу
           Db
       661 GTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTAAGG--TTTCGCCTTAGCGCCNAC 604
Qу
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Qу
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Db
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Qу
          Db
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Qу
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Qу
          Db
       387 GTGCGGCAGCTGTACATTAACTTCCGCAAGGACCTCGGCTGGGAGTGGATCCACGAGCCC 328
Qу
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Db
      Qу
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Db	209	TGC-GCGTGCCGCAGGCGCTGGAGCCCCTTCGTGTACTACGTGGGCCGCAAGCCC	151
Qy	1147	AAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTG 1196	
Db	150		

Search completed: October 28, 2003, 00:08:04 Job time : 2979.42 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 19:11:58; Search time 33.2026 Seconds

(without alignments)

1902.657 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:\*

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4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

		•			DO:::21:(2	
		ફ				
Result		Query	T	D.D.	TD	Dan musicat dan
No.	Score	Match	Length :	DR	ID	Description
1	2053	97.1	390	23	AAE13596	Porcine transformi
2	1931	91.3	390	22	AAM39186	Human polypeptide
3	1924	91.0	390	7	AAP61468	PreTGF-beta gene p
4	1924	91.0	390	11	AAR04034	Sequence of pre-TG
5	1924	91.0	390	11	AAR05258	Human pre-transfor
6	1924	91.0	390	12	AAR13813	Human pro-TGF-beta
7	1924	91.0	390	16	AAR73596	Human TGF-beta 1 p
8	1924	91.0	390	17	AAR90827	Pre-transforming g
9	1921	90.9	390	23	AAU77101	Human transforming
10	1921	90.9	390	23	AAE16943	Human transforming
11	1920.5	90.8	391	24	ABB82780	TGFB1 Arg25Pro pol
12	1919	90.8	390	13	AAR20124	Sequence of simian
13	1915	90.6	390	15	AAR46227	Human pre-TGF-beta
14	1913.5	90.5	391	16	AAR83054	Transforming growt
15	1913	90.5	390	19	AAW78785	Human pre-transfor
16	1912	90.4	390	22	AAB84601	Nucleotide sequenc
17	1909.5	90.3	391	9	AAP81362	Human transforming
18	1908.5	90.3	434	11	AAR03743	Monkey transformin
19	1905	90.1	390	24	ABB82781	TGFB1 Arg25Pro pol
20	1888	89.3	386	11	AAR05663	Simian Transformin
21	1882.5	89.0	387	11	AAR05664	Simian Transformin
22	1872	88.6	390	11	AAR05492	Chimeric simian TG
23	1868	88.4	390	13	AAR27522	TGF-beta 1/beta 2
24	1848.5	87.4	389	13	AAR29657	TGF-beta 1. Homo
25	1843.5	87.2	453	22	AAM40972	Human polypeptide
26	1763	83.4	390	13	AAR20126	Sequence of hybrid
27	1762	83.3	390	11	AAR05749	Human TGF-Beta2 ex
28	1756	83.1	390	11	AAR05665	Human Transforming
29	1754	83.0	390	11	AAR05666	Hybrid transformin
30	1746.5	82.6	391	10	AAP91900	Sequence encoded b
31	1718.5	81.3	389	16	AAR79921	Simian-human hybri
32	1300	61.5	278	15	AAR53090	Polypeptide cross-
33	1295	61.3	278	12	AAR12541	Latency associated
34	1262.5	59.7	458	23	ABG31507	LAP-mIFNB construc
35	1262.5	59.7	463	23	ABG31510	LAP-huIFNB constru
36	1173.5	55.5	290	22	ABG06792	Novel human diagno
37	1135	53.7	450	23	ABG31508	mIFNB-LAP construc
38	1118	52.9	448	23	ABG31509	huIFNB-LAP constru
39 40	9 <b>44</b> 902.5	44.7 42.7	227 236	22 22	ABG20234	Novel human diagno
	873				ABG20233	Novel human diagno
41 42	873	41.3 41.3	382 382	21 23	AAB08338	Amino acid sequenc Frog transforming
43	837	39.6	362 456	19	AAU77105 AAW78786	Pig transforming g
44	836	39.5	412	16	AAR73598	Human TGF-beta 3 p
45	832	39.4	412	13	AAR20621	Transforming Growt
±2	0,52	٠,٠٠٠	7.12	13	AARZUUZI	Transforming Growt

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RESULT 1
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ΙD
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XX
AC
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ХX
DT
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     Porcine transforming growth factor beta 1 (TGF-beta1) mutant.
ХX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW
KW
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
KW
     mutein.
XX
OS
     Sus scrofa.
XX
FΗ
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FT
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XX
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PF
XX
PR
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XX
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PΑ
ХX
     Strober W, Nakamura K, Kitani A, Fuss IJ;
ΡI
XX
    WPI; 2002-026155/03.
DR
DR
     N-PSDB; AAD22696.
XX
PT
     Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
     disease in humans, comprises vector containing transforming growth
PT
     factor-beta under the control of inducible promoter -
XX
PS
     Example 1; Fig 1; 78pp; English.
XX
CC
     The invention relates to a composition containing a vector comprising a
CC
     gene encoding a regulatory transcription factor under the control of a
CC
     promoter encoding a transforming growth factor-beta (TGF-beta). The
     vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta2
CC
     or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
CC
     is part of a host suspected of having an autoimmune disease, especially
CC
     inflammatory bowel disease (IBD), under conditions such that the
CC
    polypeptide encoded by the nucleic acid sequence in the vector is
CC
     expressed. The vector is delivered using a delivery system. The delivery
CC
     of the vector results in substantial elimination of symptoms of the
CC
     autoimmune disease and increased production of IL-10 by the host. The
CC
     composition is useful for treating various diseases with an autoimmune
```

```
component such as multiple sclerosis, rheumatoid arthritis, systemic
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
    The vector is further useful for screening of the effect of test
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
CC
    The present sequence is porcine TGF-betal mutant.
XX
SO
    Sequence
            390 AA;
                      97.1%; Score 2053; DB 23; Length 390;
 Query Match
 Best Local Similarity
                      98.0%; Pred. No. 1.3e-174;
 Matches 390; Conservative
                            0; Mismatches
                                           0:
                                              Indels
                                                       8: Gaps
                                                                 1;
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Qу
            Db
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Qу
            Db
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Qу
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEOHVELYOKYSNDSWR 180
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Qу
            1111111111111
Db
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        301 CCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
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            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
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Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
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XX
AC
    AAM39186;
XX
DT
    22-OCT-2001 (first entry)
XX
DE
    Human polypeptide SEO ID NO 2331.
XX
KW
    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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KW
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KW
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KW
KW
    chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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CC

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KW
     leukaemia.
XX
OS
     Homo sapiens.
XX
PN
     WO200153312-A1.
XX
PD
     26-JUL-2001.
XX
ΡF
     26-DEC-2000; 2000WO-US34263.
XX
PR
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
PR
     09-JUL-2000; 2000US-0598042.
     19-JUL-2000; 2000US-0620312.
PR
PR
     03-AUG-2000; 2000US-0653450.
PR
     14-SEP-2000; 2000US-0662191.
PR
     19-OCT-2000; 2000US-0693036.
PR
     29-NOV-2000; 2000US-0727344.
XX
PΑ
     (HYSE-) HYSEQ INC.
XX
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y,
PΙ
                                                              Ren F, Wang D;
PΙ
                                                              Zhang J;
ΡI
     Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR
     WPI; 2001-442253/47.
DR
     N-PSDB; AAI58342.
XX
PT
     Novel nucleic acids and polypeptides, useful for treating disorders
PT
     such as central nervous system injuries -
XX
PS
     Example 4; SEQ ID NO 2331; 10078pp; English.
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
CC
     of the invention may be used to treat diseases of the peripheral nervous
CC
     system, such as peripheral nervous injuries, peripheral neuropathy and
CC
     localised neuropathies and central nervous system diseases, such as
CC
     Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC
     lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
     utilisation of the activities such as: Immune system suppression,
CC
     Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
     and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC
     assays for receptor activity, arthritis and inflammation, leukaemias and
CC
     C.N.S disorders.
CC
     Note: The sequence data for this patent did not form part of the printed
CC
     specification.
XX
SQ
     Sequence
                390 AA;
  Query Match
                           91.3%; Score 1931; DB 22; Length 390;
                          92.0%; Pred. No. 1e-163;
 Best Local Similarity
 Matches 366; Conservative 10; Mismatches
                                                   14;
                                                        Indels
```

Qу

```
1 MPPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
        61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
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Qу
           Db
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        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qy
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 3
AAP61468
ΙD
    AAP61468 standard; Protein; 390 AA.
XX
AC
   AAP61468;
XX
DT
    31-OCT-2002
              (updated)
DT
    28-OCT-1991
              (first entry)
XX
DE
    PreTGF-beta gene product.
XX
KW
    Transforming growth factor beta; cancer; wound healing.
XX
OS
    Unidentified.
XX
FΗ
    Key
                Location/Qualifiers
FT
    Protein
                279..390
XX
PN
    EP200341-A.
XX
PD
    10-DEC-1986.
XX
PF
    21-MAR-1986;
               86EP-0302112.
XX
PR
    22-MAR-1985;
               85US-0715142.
PR
    13-MAR-1987;
               87US-0025423.
XX
    (GETH ) GENENTECH INC.
PA
XX
```

```
PΙ
    Derynck RMA;
XX
DR
    WPI; 1986-326875/50.
DR
    N-PSDB: AAN60972.
XX
PT
    TGF-beta prodn. from transformed hosts - useful esp. for treating
PT
    wounds (J6 2/9/86).
XX
PS
    Disclosure; Fig 1b; 26pp; English.
XX
CC
    The gene product is known to stimulate cell proliferation and
CC
    inhibit anchorage-dependent growth of a variety of human cancer cell
CC
    lines, it is esp. useful in treatment of burns and the promotion of
CC
    surface and internal wound healing. TGF-beta may be expressed from a
    transformed CHO cell line.
CC
CC
    (Updated on 31-OCT-2002 to add missing OS field.)
XX
SO
    Sequence
             390 AA;
 Query Match
                     91.0%; Score 1924; DB 7; Length 390;
                     91.7%; Pred. No. 4.4e-163;
 Best Local Similarity
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                     8; Gaps
                                                               1;
Qу
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            Db
          1 MPPSGLRLLPLLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Оy
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
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Dh
Qу
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Db
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        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR------ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 4
AAR04034
    AAR04034 standard; protein; 390 AA.
ID
XX
AC
    AAR04034;
```

```
DT
     25-MAR-2003
                 (updated)
DT
     31-OCT-2002
                 (updated)
DT
     31-MAY-1989
                 (first entry)
XX
DE
    Sequence of pre-TGF-beta 1.
XX
KW
     Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
     inhibition.
XX
OS
    Homo sapiens.
XX
FΗ
     Key
                   Location/Oualifiers
FT
     CDS
                   348..500
XX
PN
    WO8912101-A.
XX
PD
    14-DEC-1989.
XX
PF
     08-JUN-1988;
                 88WO-US01945.
XX
PR
    08-JUN-1988;
                  88WO-US01945.
XX
PΑ
     (GETH ) GENENTECH INC.
XX
PΙ
    Dernyck RMA, Goeddel DV;
XX
DR
    WPI; 1990-007474/01.
DR
    N-PSDB; AAQ02815.
XX
PT
    Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT
    probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PΤ
    and neoplastic cells, eg A549.
XX
PS
    Disclosure; Fig. 2; 61pp; English.
XX
CC
    Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta
CC
    1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The
    nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful
CC
CC
    as a probe or to produce TGF-beta 3 for inhibition of normal and
CC
    neoplastic cell growth.
CC
     (Updated on 31-OCT-2002 to add missing OS field.)
CC
     (Updated on 25-MAR-2003 to correct PR field.)
CC
     (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ
    Sequence
               390 AA;
  Query Match
                        91.0%; Score 1924; DB 11; Length 390;
 Best Local Similarity
                        91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches
                                                             8; Gaps
                                               15; Indels
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
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XX

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Db
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QУ
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 5
AAR05258
    AAR05258 standard; protein; 390 AA.
TD
XX
AC
    AAR05258;
XX
DT
    25-MAR-2003 (updated)
    05-AUG-1990 (first entry)
DT
XX
DE
    Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
XX
KW
    Transforming growth factor-beta-1 (TGF-beta-1);
KW
    neoplastic cell line inhibition;
KW
    EGF-potentiated anchorage-independent growth.
XX
OS
    Homo sapiens.
XX
FH
    Key
                  Location/Qualifiers
FT
    Peptide
                  1..278
FT
    Protein
                  279..2011
FT
    Domain
                  8..23
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                  /note="hydrophobic domain"
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                  82..84
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                  /note="potential N-glycosylation site "
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    Modified-site
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FT
                  /note="as above"
FT
                  176..178
    Modified-site
                  /note="as above"
FT
FT
    Cleavage-site
                  277..278
FT
                  /note="proteolytic cleavage site"
XX
    US4886747-A.
PN
XX
PD
    12-DEC-1989.
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XX
ΡF
    13-MAR-1987;
                 87US-0025423.
XX
    13-MAR-1987; 87US-0025423.
PR
PR
    22-MAR-1985;
                85US-0715142.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA, Goeddel DV;
XX
    WPI; 1990-051338/07.
DR
    N-PSDB; AAQ93301.
DR
XX
PT
    Nucleic acid encoding transforming growth factor-beta -
    cloned into expression vectors for expression in eukaryotic host
PT
PT
    cells for therapeutic use
XX
    Disclosure; Fig 1b; 28pp; English.
PS
XX
CC
    Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-transitional
CC
    cleavage of the precursor gives rise to the mature TGF-beta monomer.
CC
    The sequence for human TGF-beta was determined by direct amino acid
CC
    sequence analysis and by deduction from the TGF-beta cDNA. It is
CC
    capable of inducing EGF-potentiated anchorage-independent growth of
    target cell lines, and/or growth inhibition of neoplastic cell lines.
CC
CC
    can be used for treating wounds, eg burns or epidermal ulcers.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
             390 AA;
SQ
    Sequence
 Query Match
                      91.0%; Score 1924; DB 11; Length 390;
 Best Local Similarity
                      91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches
                                           15; Indels
                                                       8; Gaps
                                                                  1;
Qу
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            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
ďŪ
QУ
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR------ALDTNYCFSSTEKN 292
Db
Qу
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            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
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Qу
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 6
AAR13813
    AAR13813 standard; Protein; 390 AA.
ID
XX
AC
    AAR13813;
XX
DT
    20-NOV-1991 (first entry)
XX
    Human pro-TGF-beta 1.
DE
XX
KW
    Osteogenetic; tumoricidal.
XX
OS
    Homo sapiens.
XX
FΗ
                    Location/Qualifiers
     Key
FT
     Peptide
                    1..29
FT
                    /note= "signal peptide"
FT
     Peptide
                    30..390
FT
                    /note= "pro-TGF-beta 1"
FT
     Peptide
                    279..390
FT
                    /note= "TGF-beta 1"
XX
    JP03180192-A.
PN
XX
PD
    06-AUG-1991.
XX
ΡF
    07-DEC-1989;
                   89JP-0318243.
XX
PR
     07-DEC-1989;
                   89JP-0318243.
XX
Aq
     (KIRI ) KIRIN BREWERY KK.
XX
DR
    WPI; 1991-271579/37.
DR
    N-PSDB; AAQ13392.
XX
PΤ
     Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT
     preparing DNA chain contg. base sequence coding for human
PΤ
     pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
     Claim 1; Fig 1; 16pp; Japanese.
XX
CC
     The amino acid sequence codes for human prepro-TGF-beta 1 which
CC
     can be produced by recombinant methods, it has osteogenetic and
CC
     tumoricidal activity.
XX
SO
    Sequence
               390 AA;
                         91.0%; Score 1924; DB 12;
  Query Match
                                                      Length 390;
                         91.7%; Pred. No. 4.4e-163;
  Best Local Similarity
  Matches 365; Conservative 10; Mismatches 15; Indels
                                                                8; Gaps
                                                                            1;
```

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1 MAPSGLRLLPLLLVLLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           Db
         1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Db
        121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
AAR73596
    AAR73596 standard; Protein; 390 AA.
ID
XX
AC
    AAR73596;
XX
DT
    25-MAR-2003
              (updated)
DT
    20-DEC-1995
              (first entry)
XX
DE
    Human TGF-beta 1 protein.
XX
KW
    Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;
KW
    TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
KW
    bone-inducing cofactor.
XX
OS
    Homo sapiens.
XX
PN
    US5409896-A.
XX
PD
    25-APR-1995.
XX
PF
    12-NOV-1993;
                93US-0132405.
XX
PR
    01-SEP-1989:
                89US-0401906.
PR
    12-NOV-1991;
                91US-0790856.
PR
    18-MAY-1993;
                93US-0063841.
PR
    12-NOV-1993;
                93US-0132405.
XX
```

```
(GETH ) GENENTECH INC.
PΑ
XX
PΙ
    Ammann AJ, Rudman CG;
XX
DR
    WPI; 1995-169610/22.
XX
PT
    Compsn. for treating skeletal tissue deficiency - comprising
PΤ
    transforming growth factor-beta and an osteogenic cell source in a
PT
    carrier
XX
PS
    Claim 3; Column 15-18; 19pp; English.
XX
CC
    This sequence represents human transforming growth factor-beta 1
CC
    (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
CC
    AAR73598) are claimed within the scope of the invention. The invention
CC
    is a composition consisting of a TGF-beta protein and an osteogenic cell
CC
    source (OCS) formulated in an acceptable carrier other than a bone
CC
    morphogenic cofactor. This composition can be used for the restoration
CC
    of bone deficiency. This provides for the generation of mature bone
    only where it is required, without the inclusion of a specific
CC
CC
    bone-inducing cofactor. This method can be used with any of the 5 human
CC
    TGF-beta's or with TGF-beta from other species.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
    Sequence 390 AA;
 Ouery Match
                      91.0%; Score 1924; DB 16; Length 390;
 Best Local Similarity 91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                       8; Gaps
                                                                 1:
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            1 MPPSGLRLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
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            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Qу
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            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKKVEQHVELYQKYSNNSWR 180
Dh
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
dQ
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            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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RESULT 8
AAR90827
     AAR90827 standard; Protein; 390 AA.
ΙD
XX
AC
     AAR90827;
XX
                  (updated)
DT
     25-MAR-2003
                  (first entry)
DT
     25-JAN-1980
XX
DE
     Pre-transforming growth factor beta 1.
XX
     transforming growth factor beta 1; wound healing;
KW
KW
     recombinant production.
XX
OS
     Homo sapiens.
XX
FΗ
                     Location/Qualifiers
     Key
FT
     Domain
                      8..23
FT
                      /note= "hydrophobic domain"
FT
     Modified-site
                      82..84
FT
                      /note= "potential N-glycosylation site"
FT
     Modified-site
                      136..138
                      /note= "potential N-glycosylation site"
FT
FT
     Modified-site
                      176..178
FT
                      /note= "potential N-glycosylation site"
FΤ
     Cleavage-site
                     277..279
                      /note= "trypsin-like peptidase cleavage site"
FT
FT
     Protein
                      279..390
FT
                      /label= mature TGF beta 1
XX
PN
     US5482851-A.
XX
PD
     09-JAN-1996.
XX
ΡF
     05-NOV-1993;
                    93US-0147364.
XX
PR
     13-MAR-1987;
                    87US-0025423.
                    85US-0715142.
PR
     22-MAR-1985;
     04-AUG-1989;
                    89US-0389929.
PR
PR
     04-MAR-1992;
                    92US-0845893.
PR
     05-NOV-1993;
                    93US-0147364.
XX
PΑ
     (GETH ) GENENTECH INC.
XX
     Derynck RMA, Goeddel DV;
ΡI
XX
DR
     WPI; 1996-076891/08.
     N-PSDB; AAT15720.
DR
XX
PΤ
     New recombinant human transforming growth factor-beta prods. - produced
     using Chinese hamster ovary cells, for use in diagnostic applications
PT
     or in therapy
PT
XX
     Example 3; Fig 1A-C; 26pp; English.
PS
XX
```

```
CC
    by AAT15720. The mature TGF beta 1 monomer is cleaved from the
CC
    precursor at the Arg-Arg dipeptide immediately preceding the mature
CC
    TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal
CC
    signal peptide typical of most secreted proteins. The pre-TGF beta 1
CC
    contains several pairs of basic residues which could undergo
CC
    post-translational cleavage and give rise to separate polypeptide
CC
    entities. The precursor contains 3 potential N-glycosylation sites, none
CC
    of which are localised in the mature TGF beta 1. This is useful in
CC
    purification of the mature protein. TGF beta 1 can be used in, e.g. wound
CC
    healing.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
             390 AA;
 Query Match
                      91.0%; Score 1924; DB 17; Length 390;
 Best Local Similarity
                     91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                      8; Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGLRLLPLLUPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Oy
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLKVEOHVELYOKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
AAU77101
ID
    AAU77101 standard; Protein; 390 AA.
XX
AC
    AAU77101:
XX
DT
    05-JUN-2002 (first entry)
XX
    Human transforming growth factor beta 1 (TFG-beta-1) polypeptide.
DE
```

The pre-transforming growth factor (TGF) beta 1 protein is encoded

CC

```
XX
KW
     Human; transforming growth factor beta; TGF-beta; insulin production;
KW
     type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
KW
     pancreatic duct tissue; ischaemia; stroke; nervous system aging;
     neurological condition; neurodegenerative disease; inflammation;
KW
KW
     vasal injury; chemical injury; traumatic injury; tumour-induced injury;
KW
     amyotrophic lateral sclerosis; spinocerebellar degeneration;
KW
     immunological disease; multiple sclerosis; TGF-beta-1.
XX
OS
     Homo sapiens.
XX
ΡN
     W0200212336-A2.
XX
PD
     14-FEB-2002.
XX
PF
     09-FEB-2001; 2001WO-US04192.
XX
PR
     09-AUG-2000; 2000US-0635368.
XX
PΑ
     (CURI-) CURIS INC.
XX
PΙ
     Wang M, Pang K;
XX
DR
     WPI; 2002-257468/30.
XX
PT
     Treating a subject with a disorder resulting from insufficient insulin
PT
     production, and inducing outgrowth of pancreatic cells, involves using
PΤ
     a transforming growth factor beta therapeutic -
XX
PS
     Disclosure; Fig 1; 77pp; English.
XX
CC
     The invention relates to treating a subject with a disorder resulting
CC
     from insufficient insulin production, involving contacting the subject
CC
     with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
CC
     polypeptides can be used for treating a subject with a disorder resulting
CC
     from insufficient insulin production, e.g. type I diabetes mellitus, and
CC
     for inducing outgrowth of pancreatic cells associated with pancreatic
CC
     duct tissue within a subject. A composition comprising a TGF-beta protein
CC
     may be useful in wound healing and treatment of neurological conditions
CC
     derived from acute, subacute or chronic injury to the nervous system,
CC
     including traumatic injury, chemical injury, vasal injury and deficits
CC
     (such as ischaemia resulting from stroke), together with
CC
     infectious/inflammatory and tumour-induced injury, aging of the nervous
     system including Alzheimer's disease, chronic neurodegenerative diseases
CC
CC
     including Parkinson's disease, Huntington's chorea, amyotrophic lateral
CC
     sclerosis, spinocerebellar degenerations and chronic immunological
CC
     diseases of the nervous system or affecting the nervous system, including
CC
     multiple sclerosis. This sequence represents the human TGF-beta-1
CC
     protein.
XX
SO
     Sequence
                390 AA;
  Query Match
                          90.9%; Score 1921; DB 23; Length 390;
                          91.7%; Pred. No. 8.1e-163;
 Best Local Similarity
 Matches 365; Conservative 10; Mismatches
                                                  15;
                                                      Indels
                                                                 8; Gaps
                                                                              1;
```

QУ

```
Db
         1 MPPSGLRLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
QУ
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 10
AAE16943
ΙD
    AAE16943 standard; Protein; 390 AA.
XX
AC
    AAE16943;
XX
DT
    18-APR-2002 (first entry)
XX
DE
    Human transforming growth factor-betal (TGF-betal) protein.
XX
KW
    Human; transforming growth factor-betal; TGF-betal; osteoporosis;
    latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
KW
    immunomodulation; inflammatory disease; fibrotic disease; cancer;
KW
KW
    diabetic retinopathy; chronic obstructive pulmonary disorder;
KW
    bone resorption; rheumatoid arthritis; psoriasis; restenosis;
KW
    atherosclerosis; liver fibrosis; asthma; cytostatic; osteopathic;
    ophthalmological; antiarteriosclerotic; vasotropic.
KW
XX
OS
    Homo sapiens.
XX
FH
    кеу
                 Location/Qualifiers
FT
    Peptide
                 1..29
FT
                 /label= Signal peptide
FT
    Region
                 30..278
                 /note= "LAP-beta1"
FT
FT
    Domain
                 244..246
FT
                 /note= "RGD motif"
                 279..390
FT
    Protein
FT
                 /note= "Human mature TGF-betal protein"
```

```
XX
ΡN
    WO200190186-A1.
XX
    29-NOV-2001.
PD
XX
    25-MAY-2001; 2001WO-GB02352.
PF
XX
    26-MAY-2000; 2000GB-0012991.
PR
    05-JAN-2001; 2001GB-0000286.
PR
XX
     (GLAX ) GLAXO GROUP LTD.
PA
XX
    Ludbrook S, Barry S, Horgan C, Miller D;
PΙ
XX
DR
    WPI; 2002-097645/13.
XX
    Identifying modulators of interactions between latency associated
PT
    peptides and integrin alphavbeta3 for therapeutics, by contacting the
PT
    peptide and integrin with a test product and determining if the product
PT
PT
    modulates interaction -
XX
PS
    Disclosure; Page 37-39; 44pp; English.
XX
CC
    The invention relates to a method for identification of a modulator
    of the interaction between latency associated peptide (LAP) of
CC
CC
    transforming growth factor-betal (TGF-betal) and integrin alphaybeta3.
    The method is useful for identifying a modulator of the interaction
CC
CC
    between LAP and integrin alphavbeta3. The method is useful for
    immunomodulation, in the treatment of inflammatory disease, fibrotic
CC
CC
    disease, cancer, diabetic retinopathy, bone resorption or osteoporosis,
CC
    and for preventing apoptosis administering the modulator to the host.
CC
    The modulator (inhibitor of the interaction between LAP-betal and
CC
    integrin alphavbeta3) is useful in the manufacture of a medicament for
CC
    immunomodulation. The modulator (activator of the interaction between
CC
    LAP-betal and integrin alphavbeta3 ) is useful in the manufacture of
CC
    medicament for preventing apoptosis. The modulator is useful for
CC
    treating a inflammatory or fibrotic disease such as chronic obstructive
CC
    pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis,
CC
    atherosclerosis, liver fibrosis and asthma. The present sequence is
CC
    human TGF-betal protein.
XX
SQ
    Sequence
               390 AA;
  Ouery Match
                        90.9%; Score 1921; DB 23; Length 390;
  Best Local Similarity 91.7%; Pred. No. 8.1e-163;
 Matches 365; Conservative 10; Mismatches
                                              15;
                                                  Indels
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
           1 MPPSGLRLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
```

```
Db
         121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
QУ
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            Db
         241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
Qу
            Dh
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
         361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
QУ
            Db
         353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 11
ABB82780
    ABB82780 standard; Protein; 391 AA.
ID
XX
AC
    ABB82780;
XX
DT
    18-MAR-2003 (first entry)
XX
DE
    TGFB1 Arg25Pro polymorphism G-allele protein sequence.
XX
KW
    Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
KW
    renal failure; nephrotropic; human; allele.
XX
OS
    Homo sapiens.
XX
PN
    WO200290585-A2.
XX
PD
    14-NOV-2002.
XX
PF
    08-MAY-2002; 2002WO-GB02066.
XX
PR
    09-MAY-2001; 2001GB-0011277.
XX
PΑ
    (UYSH-) UNIV SHEFFIELD HALLAM.
XX
ΡI
    El-Nahas AM, Blakemore A, Khalil MS;
XX
DR
    WPI; 2003-120560/11.
    N-PSDB; ABV75391.
DR
XX
PT
    Determining an individual's susceptibility to the progression of renal
PT
    failure comprises detecting the presence of a genetic polymorphism
    pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
PT
PT
    from the individual
XX
PS
    Claim 51; Page 59-61; 62pp; English.
XX
    The invention relates to determining an individual's susceptibility to
CC
```

```
renal failure and invovles detecting the presence of a genetic
CC
    polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
CC
    a sample from an individual, where polymorphism pattern is associated
CC
    with renal failure. The method is useful for determining an individual's
CC
    susceptibility to the progression of renal failure. The nucleic acid
CC
    comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
CC
    comprising a sequence of 391 amino acids is useful for preparing a
CC
    medicament for retarding or preventing the progression of renal disease,
CC
    and for drug research purposes for retarding or preventing the
CC
    progression of renal disease. Sequences ABV75386-88 represents the
CC
    protein sequence for the TGFB1 G-allele of the Arg25Pro polymorphism
CC
    of exon 1.
XX
SO
    Sequence
             391 AA;
                      90.8%; Score 1920.5; DB 24; Length 391;
 Query Match
                      91.7%; Pred. No. 9e-163;
 Best Local Similarity
 Matches 366; Conservative 10; Mismatches 14; Indels
                                                       9; Gaps
                                                                 2;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEOHVELYOKYSNNSW 180
Dh
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
             241 TTGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEK 292
Db
        300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
Qу
            293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 352
Db
        360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
QУ
            353 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Db
RESULT 12
    AAR20124 standard; Protein; 390 AA.
TD
XX
AC
    AAR20124;
XX
DT
    25-MAR-2003
               (updated)
               (first entry)
DT
    16-APR-1992
XX
```

CC

```
XX
KW
    Hypertension therapy; hypotensive agent; blood pressure modulator.
XX
OS
    Monkey.
XX
FH
    Key
                  Location/Qualifiers
FT
    Peptide
                   8..21
FT
    Protein
                   279..390
XX
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
                91WO-US04449.
XX
PR
    20-JUN-1990;
                90US-0541221.
XX
PΑ
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PΙ
    Oleson FB, Comereski CR;
XX
DR
    WPI; 1992-024199/03.
DR
    N-PSDB; AAQ20289.
XX
PT
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PΤ
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
    Sequence
SO
              390 AA;
 Query Match
                       90.8%; Score 1919; DB 13; Length 390;
 Best Local Similarity 91.5%; Pred. No. 1.2e-162;
 Matches 364; Conservative 10; Mismatches 16; Indels
                                                           8; Gaps
                                                                      1;
QУ
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             1 MPPSGLKLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60
dG
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
          61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Qу
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
             Db
         121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
```

Sequence of simian transforming growth factor (TGF) beta-1.

DE

```
181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qy
            353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
RESULT 13
AAR46227
    AAR46227 standard; Protein; 390 AA.
XX
AC
    AAR46227;
XX
DT
    25-MAR-2003 (updated)
DT
    09-JUL-1994 (first entry)
XX
DE
    Human pre-TGF-beta-1.
XX
KW
    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
    transforming growth factor beta-3; recombinant; wound healing;
KW
KW
    vulnerary.
XX
OS
    Homo sapiens.
XX
                  Location/Qualifiers
FH
    Key
FT
    Peptide
                  279..390
FT
                  /label = Mat peptide
FT
                  279
    Cleavage-site
FT
                  /note= "TGF-beta-1 release site"
FT
    Modified-site
                  82..84
                  /label= N-glycosylation_site
FT
FT
    Modified-site
                  136..138
                   /label= N-glycosylation site
FT
FT
    Modified-site
                  176..178
FT
                  /label= N-glycosylation site
XX
PN
    US5284763-A.
XX
PD
    08-FEB-1994.
XX
PF
    04-MAR-1992;
                92US-0845893.
XX
PR
    22-MAR-1985;
                 85US-0715142.
PR
    13-MAR-1987;
                 87US-0025423.
PR
    04-AUG-1989;
                 89US-0389929.
PR
    04-MAR-1992;
                 92US-0845893.
```

```
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynk RMA, Goeddel DV;
XX
DR
    WPI; 1994-056343/07.
DR
    N-PSDB; AAQ56923.
XX
PT
    Nucleic acid sequences encoding transforming growth factor-beta -
PT
    diagnostic probes, and for use in therapeutics
XX
PS
    Disclosure; Fig 1b; 25pp; English.
XX
CC
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
    pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
CC
    respectively). A genomic fragment corresponding to a human TGF-
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
    beta.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
    Sequence 390 AA;
SO
 Query Match
                      90.6%; Score 1915; DB 15; Length 390;
 Best Local Similarity 91.5%; Pred. No. 2.8e-162;
 Matches 364; Conservative 10; Mismatches 16; Indels
                                                       8; Gaps
                                                                 1:
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLVLLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEREPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                       Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            11111111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Qу
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XX
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XX
DT
     25-JUN-1996 (first entry)
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     Transforming growth factor-beta 1.
XX
KW
     macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW
     interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
     nitric oxide production; hypotension; inflammation; septic shock;
KW
KW
     treatment.
XX
OS
     Mammalian sp.
XX
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     12-OCT-1995.
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PF
     05-APR-1994;
                    94WO-US03705.
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PR
     05-APR-1994;
                   94WO-US03705.
XX
PΑ
     (HARD ) HARVARD COLLEGE.
XX
PΙ
     Lee M, Perrella MA;
XX
DR
     WPI; 1995-358443/46.
     N-PSDB; AAT05876.
DR
XX
PT
     Treatment of hypotension, esp. in septic shock - by administering
PT
     transforming growth factor-beta e.g. to inhibit inducible nitric
PΤ
     oxide synthase gene transcription
XX
PS
     Disclosure; Fig 17; 52pp; English.
XX
CC
     Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit
CC
     inducible nitric oxide synthase (iNOS) gene transcription, esp. in
CC
     interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
CC
     a dose which does not inhibit consitutive NOS. TGF-beta 1 or 2
CC
     (AAR83055) or their active fragments (esp. derived from the
CC
     carboxy-terminal 112 amino acids), can be used in the treatment of
CC
     hypotension, such as that associated with severe inflammation or septic
CC
     shock.
XX
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     Sequence
                391 AA;
                          90.5%; Score 1913.5; DB 16; Length 391; 91.5%; Pred. No. 3.8e-162;
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    25-MAR-2003
               (updated)
DT
    21-DEC-1998
              (first entry)
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    30-MAY-1995; 95US-0454468.
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    (GETH ) GENENTECH INC.
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    Derynck RMA, Goeddel DV;
XX
DR
    WPI; 1998-494840/42.
    N-PSDB; AAV52933.
DR
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PT
    DNA encoding transforming growth factor-beta precursor sequence -
PT
    useful for analysis to perform manipulations to increase yield of
PT
    recombinant production of the protein
XX
PS
    Example 3; Fig 1B 1-3; 26pp; English.
XX
CC
    This is the amino acid sequence of human transforming growth
CC
    factor-beta 1 precursor (preTGF-beta 1). It was deduced from
CC
    a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates
CC
    to the recombinant production of TGF-beta. Biologically active
CC
    TGF-beta is defined as being capable of inducing EGF-potentiated
CC
    anchorage independent growth of target cell lines and/or growth
CC
    inhibition of neoplastic cell lines. Nucleic acids encoding
CC
    TGF-beta have been isolated and cloned into vectors which are
CC
    replicated in bacteria and expressed in eukaryotic cells. TGF-beta
CC
    recovered from transformed cells is used in known therapeutic
CC
    applications.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
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              390 AA;
 Query Match
                        90.5%; Score 1913; DB 19;
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Run on:		October 28, 2003, 09:09:54; Search time 24.1473 Seconds (without alignments) 2760.110 Million cell updates/sec						
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## SUMMARIES

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1	2035	96.3	390	11	US-09-214-592-26	Sequence 26, Appl
2	1934	91.5	390	11	US-09-214-592-29	Sequence 29, Appl
3	1931	91.3	390	15	US-10-087-268-2	Sequence 2, Appli
4	1924	91.0	390	15	US-10-087-268-5	Sequence 5, Appli
5	1921	90.9	390	12	US-10-276-947-1	Sequence 1, Appli
6	1919	90.8	390	11	US-09-214-592-33	Sequence 33, Appl
7	1913.5	90.5	391	11	US-09-214-592-17	Sequence 17, Appl
8	1910	90.4	390	10	US-09-756-283A-23	Sequence 23, Appl
9	1898	89.8	390	11	US-09-214-592-28	Sequence 28, Appl
10	1840	87.0	390	11	US-09-214-592-20	Sequence 20, Appl
11	1840	87.0	390	11	US-09-214-592-23	Sequence 23, Appl
12	1577	74.6	315	11	US-09-214-592-25	Sequence 25, Appl
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14	1139	53.9	447	10	US-09-756-283A-22	Sequence 22, Appl
15	1059.5	50.1	373	11	US-09-214-592-32	Sequence 32, Appl
16	876	41.4	412	11	US-09-214-592-31	Sequence 31, Appl
17	873	41.3	382	11	US-09-214-592-34	Sequence 34, Appl
18	872.5	41.3	383	10	US-09-756-283A-27	Sequence 27, Appl
19	838.5	39.7	409	11	US-09-214-592-27	Sequence 27, Appl
20	835	39.5	410	11	US-09-214-592-22	Sequence 22, Appl
21	834	39.5	412	11	US-09-214-592-24	Sequence 24, Appl
22	832	39.4	412	11	US-09-214-592-19	Sequence 19, Appl
23	832	39.4	412	14	US-10-028-158-21	Sequence 21, Appl
24	831.5	39.3	414	11	US-09-214-592-21	Sequence 21, Appl
25	828	39.2	412	10	US-09-756-283A-25	Sequence 25, Appl
26	816.5	38.6	414	10	US-09-756-283A-24	Sequence 24, Appl
27	816.5	38.6	414	11	US-09-214-592-18	Sequence 18, Appl
28	815.5	38.6	412	11	US-09-214-592-30	Sequence 30, Appl
29	804.5	38.1	304	10	US-09-756-283A-26	Sequence 26, Appl
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31	642	30.4	115	10	US-09-859-211-47	Sequence 47, Appl
32	642	30.4	115	10	US-09-880-708-25	Sequence 25, Appl
33	642	30.4	115	11	US-09-872-856-47	Sequence 47, Appl
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## ALIGNMENTS

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RESULT 1
US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
 CURRENT APPLICATION NUMBER: US/09/214,592A
 CURRENT FILING DATE: 1999-01-18
 NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 26
   LENGTH: 390
   TYPE: PRT
   ORGANISM: porcine
US-09-214-592-26
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; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
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US-09-214-592-29
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US-10-087-268-2
; Sequence 2, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
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   ORGANISM: Human
US-10-087-268-2
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; Publication No. US20030119010A1
; GENERAL INFORMATION:
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  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
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 FILE REFERENCE: Fibrosis
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 CURRENT FILING DATE: 2002-03-01
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 Best Local Similarity 91.7%; Pred. No. 5.1e-172;
 Matches 365; Conservative 10; Mismatches
                                       15; Indels
                                                       Gaps
Qу
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
           1 MPPSGLRLLPLLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
        61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           11111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
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RESULT 5
US-10-276-947-1
; Sequence 1, Application US/10276947
; Publication No. US20030176315A1
; GENERAL INFORMATION:
  APPLICANT: GLAXO GROUP LIMITED
  TITLE OF INVENTION: MEDICAL PRODUCTS
  FILE REFERENCE: PG3949
  CURRENT APPLICATION NUMBER: US/10/276,947
  CURRENT FILING DATE: 2002-11-21
  PRIOR APPLICATION NUMBER: GB 0012991.6
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: GB 0100286.4
  PRIOR FILING DATE: 2001-01-05
  NUMBER OF SEQ ID NOS: 1
  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-276-947-1
 Query Match
                     90.9%; Score 1921; DB 12; Length 390;
 Best Local Similarity 91.7%; Pred. No. 9.8e-172;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                     8; Gaps
                                                               1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             Db
          1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           11111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
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```
RESULT 6
US-09-214-592-33
; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 33
   LENGTH: 390
   TYPE: PRT
   ORGANISM: simian
US-09-214-592-33
 Query Match
                     90.8%; Score 1919; DB 11; Length 390;
 Best Local Similarity
                     91.5%; Pred. No. 1.5e-171;
 Matches 364; Conservative 10; Mismatches
                                        16; Indels
                                                     8; Gaps
                                                               1:
Qу
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
           Db
         1 MPPSGLRLLPLLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
           121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           Db
        181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           111111111111
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Dh
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
QУ
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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```
US-09-214-592-17
; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
 SOFTWARE:
; SEQ ID NO 17
   LENGTH: 391
   TYPE: PRT
   ORGANISM: human
US-09-214-592-17
 Query Match
                     90.5%; Score 1913.5; DB 11; Length 391;
 Best Local Similarity 91.5%; Pred. No. 5e-171;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                   9; Gaps
                                                              2;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           1 MPPSGLRLLPLLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
        61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
           181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
            241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEK 292
Db
        300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
Qу
           Db
        293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGAS 352
        360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Db
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; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-756-283A-23
                     90.4%; Score 1910; DB 10; Length 390;
 Query Match
                     91.2%; Pred. No. 1.1e-170;
 Best Local Similarity
 Matches 363; Conservative 10; Mismatches 17; Indels
                                                    8; Gaps
                                                               1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
           1 MPPSGLRLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHHEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Dh
        121 YDKFKQSTHSTYMFFNISELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           1111111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLQSSRHRR-----ALDTNYCFSSTEKN 292
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
US-09-214-592-28
; Sequence 28, Application US/09214592A
: Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
```

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APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 28
   LENGTH: 390
   TYPE: PRT
   ORGANISM: canine
US-09-214-592-28
 Query Match
                     89.8%; Score 1898; DB 11; Length 390;
 Best Local Similarity 90.7%; Pred. No. 1.4e-169;
 Matches 361; Conservative 12; Mismatches
                                        17; Indels
                                                     8; Gaps
                                                               1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
QУ
           Db
         1 MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEOHVELYOKYSNDSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
             241 SSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRORR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 10
US-09-214-592-20
; Sequence 20, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
; APPLICANT: Sato, CYasufumi
```

```
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 20
   LENGTH: 390
   TYPE: PRT
   ORGANISM: murine
US-09-214-592-20
 Query Match
                      87.0%; Score 1840; DB 11; Length 390;
 Best Local Similarity
                      86.9%; Pred. No. 3.9e-164;
 Matches 346; Conservative 15; Mismatches
                                          29; Indels
                                                      8: Gaps
                                                                 1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            Db
          1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
                  |\cdot|
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLORLKSSVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
             1111111111111
Db
        241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 11
US-09-214-592-23
; Sequence 23, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
```

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TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: rat
US-09-214-592-23
 Query Match
                     87.0%; Score 1840; DB 11; Length 390;
 Best Local Similarity 86.9%; Pred. No. 3.9e-164;
 Matches 346; Conservative 14; Mismatches
                                         30; Indels
                                                      8; Gaps
                                                                1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
QУ
            1 MPPSGLRLLPLLLPLPULLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
QУ
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
                  Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Dh
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
             241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
QУ
           353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 12
US-09-214-592-25
; Sequence 25, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
 FILE REFERENCE: 11060
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CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 25
   LENGTH: 315
   TYPE: PRT
   ORGANISM: bovine
US-09-214-592-25
 Query Match
                     74.6%; Score 1577; DB 11; Length 315;
 Best Local Similarity 91.3%; Pred. No. 1.4e-139;
                           9; Mismatches 11; Indels
 Matches 295; Conservative
                                                      8; Gaps
                                                                1:
         76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
Qу
            Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
        136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
Qу
            Db
         61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            Db
        121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
        256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
                                     Db
        181 PFLLLMATPLERAQHLHSSRHRR------ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
        316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
            233 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 292
Dh
        376 YYVGRKPKVEOLSNMIVRSCKCS 398
QУ
            Dh
        293 YYVGRKPKVEOLSNMIVRSCKCS 315
RESULT 13
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
 APPLICANT: Chernajovsky, Yuti
 APPLICANT: Dreja, Hanna Stina
 APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
   LENGTH: 455
   TYPE: PRT
   ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/214,592A

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FEATURE:
   OTHER INFORMATION: LAP-mIFN
                            construct
US-09-756-283A-20
                     59.7%; Score 1262.5; DB 10; Length 455;
 Query Match
 Best Local Similarity 90.5%; Pred. No. 8.2e-110;
 Matches 248; Conservative 10; Mismatches
                                         15; Indels
                                                      1; Gaps
                                                                1:
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEOHVELYOKYSNDSW 179
Qу
            Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
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        181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
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        241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQS 274
RESULT 14
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
   LENGTH: 447
   TYPE: PRT
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: mIFN -LAP construct
US-09-756-283A-22
 Query Match
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 Best Local Similarity
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         14 PL-LWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGP 72
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        190 PLGLW----AGGGSAAALSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSQGEVPPGP 245
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        133 MLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSD 191
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        192 SPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIH 251
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        252 GMNRPFLLLMATPLERAOHLHS 273
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            426 GMNRPFLLLMATPLERAQHLOS 447
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RESULT 15
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
 NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 32
   LENGTH: 373
   TYPE: PRT
   ORGANISM: chicken
US-09-214-592-32
                      50.1%; Score 1059.5; DB 11; Length 373;
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 Best Local Similarity 54.5%; Pred. No. 7e-91;
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         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
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         90 GES-VEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
              :: | |:
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         62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
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204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258 Qу Db 181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239 259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316 QУ Db 240 LAMALPAERANELHSARRRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLOW 291 317 KWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVY 376 Qу 292 KWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDPLPIIY 351 Dh 377 YVGRKPKVEQLSNMIVRSCKCS 398 Qу 

Search completed: October 28, 2003, 09:27:59

352 YVGRNVRVEQLSNMVVRACKCS 373

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:37:16; Search time 13.1517 Seconds

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(without alignments)

2910.285 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Job time : 25.1473 secs

Db

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result. Query Score Match Length DB ID No. Description 96.4 390 2 A27512 2038 1 transforming growt 2 2006.5 94.9 391 2 501413 transforming growt 1934 91.5 390 2 I46463 3 transforming growt 1921 90.9 390 1 WFHU2 transforming growt 4 5 1919 90.8 390 2 A26960 transforming growt 89.8 390 2 JC4023 6 1898 transforming growt 7 87.0 390 1 WFMS2 1840 transforming growt 8 1840 87.0 390 2 S10219 transforming growt 9 1577 74.6 315 2 A40057 transforming growt 10 1059.5 50.1 373 2 A41918 transforming growt 11 876 41.4 412 2 A34939 transforming growt 12 873 41.3 382 2 B61036 transforming growt 409 2 S01825 13 838.5 39.7 transforming growt 410 2 A41397 835 39.5 14 transforming growt 410 2 A55706 39.5 15 834 transforming growt 16 832 39.4 412 2 A36169 transforming growt 17 831.5 39.3 414 1 WFMSB2 transforming growt 18 816.5 38.6 414 1 WFMKB2 transforming growt 19 816.5 38.6 414 2 A31249 transforming growt 816 38.6 413 1 WFXLB2 20 transforming growt 21 38.6 412 2 A39489 815.5 transforming growt 442 2 B31249 22 800.5 37.9 transforming growt 23 696 32.9 130 2 148196 transforming growt 24 482 22.8 112 2 A61439 transforming growt 25 281.5 13.3 425 2 I47072 inhibin beta-A cha 26 278 13.2 424 1 WFPGBA inhibin beta-A cha 277 13.1 424 1 S31440 276.5 13.1 425 1 S50898 275 13.0 426 1 B24248 27 inhibin beta-A cha 276.5 28 inhibin beta-A cha 29 275 13.0 inhibin beta-A cha 30 273 12.9 424 1 B40905 inhibin beta-A cha 31 265 12.5 398 2 JH0688 bone morphogenetic 12.5 398 2 JH0687 32 263.5 bone morphogenetic 33 260.5 12.3 394 2 S45355 bone morphogenetic 259.5 12.3 396 1 BMHU2 34 bone morphogenetic 12.3 413 2 JC4862 35 259 activin beta-A cha 257 12.2 513 1 BMHU6 36 bone morphogenetic 37 255.5 12.1 510 2 A54798 Vg-1-related prote 11.9 38 252 393 2 S37073 bone morphogenetic 239.5 39 11.3 350 2 JC5241 activin beta E cha 40 239.5 11.3 420 2 149541 bone morphogenetic 237.5 11.2 41 455 2 A43918 TGF-beta-related p 232.5 408 2 JH0801 42 11.0 bone morphogenetic 402 2 A45056 43 232 11.0 osteogenic protein 408 2 538343 44 231.5 11.0 bone morphogenetic 10.9 367 2 JC4151 45 230.5 activin beta D cha

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transforming growth factor beta-1 precursor - pig
N; Alternate names: TGF-beta
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text change 16-Jul-1999
C; Accession: A27512; A26356; I46657
R; Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A; Title: Sequence of the porcine transforming growth factor-beta precursor.
A; Reference number: A27512; MUID: 87174844; PMID: 3470708
A; Accession: A27512
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
R; Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.;
Lucas, R.; Massaque, J.
Cell 48, 409-415, 1987
A; Title: The transforming growth factor-beta system, a complex pattern of cross-
reactive ligands and receptors.
A; Reference number: A90890; MUID: 87102890; PMID: 2879635
A; Accession: A26356
A; Molecule type: protein
A; Residues: 279-322 < CHE>
R; Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn,
M.B.; Roberts, A.B.
J. Biol. Chem. 263, 18313-18317, 1988
A; Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation.
A; Reference number: I46657; MUID: 89054010; PMID: 2461367
A; Accession: I46657
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < KON>
A; Cross-references: GB: M23703; NID: q755044; PIDN: AAA64616.1; PID: q755045
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A; Gene: TGFB; TGF-beta-1
C; Superfamily: inhibin
C: Keywords: growth factor
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A27512

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transforming growth factor beta-1 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 24-Nov-1999
C:Accession: S01413
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A; Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-
A; Reference number: S01413; MUID: 88335639; PMID: 3166520
A; Accession: S01413
A; Molecule type: DNA
A; Residues: 1-391 < JAK>
A; Cross-references: EMBL: X12373; NID: q63808; PIDN: CAA30933.1; PID: q63809
C; Superfamily: inhibin
C; Keywords: growth factor
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transforming growth factor beta-1 - sheep
C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 24-Nov-1999
C; Accession: I46463; S45115
R; Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373, 1994
A; Title: Sequence and chromosomal localisation of the gene encoding ovine latent
transforming growth factor-beta 1.
A; Reference number: I46463; MUID: 95121932; PMID: 7821809
A; Accession: I46463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < WOO>
A; Cross-references: EMBL: X76916; NID: g496648; PIDN: CAA54242.1; PID: g496649
A; Note: submitted to the EMBL Data Library, December 1993
C; Superfamily: inhibin
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 Best Local Similarity 91.7%; Pred. No. 1.9e-147;
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WFHU2
transforming growth factor beta-1 precursor [validated] - human
N; Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C: Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text change 08-Dec-2000
C; Accession: A27513; A01395; A22290; I59664; S53444
R; Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A; Title: Intron-exon structure of the human transforming growth factor-beta
precursor gene.
A; Reference number: A27513; MUID: 87174845; PMID: 3470709
A; Accession: A27513
A; Molecule type: DNA
A; Residues: 1-390 < DER >
A; Cross-references: GB: X05839; GB: Y00112; NID: q37097; PIDN: CAA29283.1;
PID:q1212989
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian,
R.K.; Roberts, A.B.; Sporn, M.B.; Goeddel, D.V.
Nature 316, 701-705, 1985
A; Title: Human transforming growth factor-beta complementary DNA sequence and
expression in normal and transformed cells.
A; Reference number: A01395; MUID: 85296301; PMID: 3861940
A; Accession: A01395
A; Molecule type: mRNA
A; Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 < DE2>
A; Cross-references: GB: X02812; GB: J05114; NID: g37092; PIDN: CAA26580.1;
PID:g37093
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
R; Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A; Title: Cellular receptors for type beta transforming growth factor. Ligand
binding and affinity labeling in human and rodent cell lines.
A; Reference number: A22290; MUID: 85131019; PMID: 2982829
A; Accession: A22290
A; Molecule type: protein
A; Residues: 279-295, 'XX', 298-301 < MAS>
R; Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.;
Urushizaki, I.; Takahashi, Y.; Ito, H.
Tumor Res. 22, 41-55, 1987
A; Title: Cloning and expression of the gene for human transforming growth
factor-beta in Escherichia coli.
A; Reference number: 159664
A; Accession: I59664
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 279-390 < RES>
A; Cross-references: GB: M38449; NID: g339557; PIDN: AAA36735.1; PID: g339558
R; Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.;
Marshak, D.R.; Haley, J.D.
Biochem. J. 305, 87-92, 1995
A; Title: Physical and biological characterization of a growth-inhibitory
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activity purified from the neuroepithelioma cell line A673.

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A; Reference number: S53444; MUID: 95126934; PMID: 7826358
A; Accession: S53444
A; Status: preliminary
A; Molecule type: protein
A; Residues: 279-297 <STA>
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C; Genetics:
A; Gene: GDB: TGFB1; TGFB
A; Cross-references: GDB:120729; OMIM:190180
A; Map position: 19q13.2-19q13.2
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
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F;19-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
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RESULT 5 A26960

transforming growth factor beta-1 precursor - green monkey C; Species: Cercopithecus aethiops (green monkey, grivet)

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C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 24-Nov-1999
C; Accession: A26960
R; Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987
A; Title: Cloning and sequence analysis of simian transforming growth factor-beta
CDNA.
A; Reference number: A26960; MUID: 87246074; PMID: 3474130
A; Accession: A26960
A; Molecule type: mRNA
A; Residues: 1-390 < SHA>
A; Cross-references: GB: M16658; NID: g176552; PIDN: AAA35369.1; PID: g176553
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-16/Domain: signal sequence #status predicted <SIG>
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                                                       8; Gaps
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
QУ
            1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGOILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSNSPEWLSFDVTGVVROWLSRGGEIEGFRLSAHCSCDSKDNTLOVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
QУ
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 6
JC4023
transforming growth factor beta-1 - dog
C; Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence revision 14-Jul-1995 #text change 24-Nov-1999
C; Accession: JC4023
R; Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
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Gene 155, 307-308, 1995

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A; Title: Cloning of a canine cDNA homologous to the human transforming growth
factor-beta 1-encoding gene.
A; Reference number: JC4023; MUID: 95237630; PMID: 7721110
A: Accession: JC4023
A; Molecule type: mRNA
A; Residues: 1-390 < MAN >
A; Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C; Comment: This factor plays a multifunctional role as a regulator of mammalian
cell growth and as a modulator of immune responses.
C:Genetics:
A;Gene: tqf-betal
C; Superfamily: inhibin
C; Keywords: growth factor; transforming protein
F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>
 Query Match
                      89.8%; Score 1898; DB 2; Length 390;
 Best Local Similarity 90.7%; Pred. No. 1.5e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels
                                                       8; Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEOHVELYOKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 SSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRORR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Dh
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
transforming growth factor beta-1 precursor - mouse
N; Alternate names: TGF type 2; TGF-beta
C; Species: Mus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 24-Nov-1999
C; Accession: A01396
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
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A; Title: The murine transforming growth factor-beta precursor.
A; Reference number: A01396; MUID: 86168129; PMID: 3007454
A; Accession: A01396
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
A; Cross-references: GB: M13177; NID: g201952; PIDN: AAA40423.1; PID: q201953
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen;
transformation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 87.0%; Score 1840; DB 1; Length 390; Best Local Similarity 86.9%; Pred. No. 6.6e-140;
 Matches 346; Conservative 15; Mismatches
                                           29:
                                               Indels
                                                        8; Gaps
                                                                   1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
QУ
            1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVROWLNOGDGIOGFRFSAHCSCDSKDNKLHVEINGIS 240
Dh
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
              241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Dh
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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C; Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text change 24-Nov-1999
C; Accession: S10219; PT0023; S02267
R; Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A; Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
A; Reference number: S10219; MUID: 90272425; PMID: 2349108
A; Accession: S10219
A; Molecule type: mRNA
A; Residues: 1-390 < QIA>
A; Cross-references: EMBL: X52498; NID: q57341; PIDN: CAA36741.1; PID: q57342
R; Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989
A; Title: Purification and structural analysis of a latent form of transforming
growth factor-beta from rat platelets.
A; Reference number: PT0023; MUID: 90036779; PMID: 2478527
A; Accession: PT0023
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 < OKA>
R; Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989
A; Title: One of two subunits of masking protein in latent TGF-beta is a part of
pro-TGF-beta.
A; Reference number: S02267; MUID: 89121078; PMID: 2914605
A; Accession: S02267
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'O', 40-42, 'X', 44 < OK2 >
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; integrin binding
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-278/Domain: propeptide #status experimental <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       87.0%; Score 1840; DB 2; Length 390; 86.9%; Pred. No. 6.6e-140;
 Query Match
 Best Local Similarity
 Matches 346; Conservative 14; Mismatches
                                             30;
                                                  Indels
                                                         8; Gaps
                                                                       1;
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
             1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
                    Db
         121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
Qу
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
             Db
         181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
QУ
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Db
          241 PKRRGDLGTIHDMNRPFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKN 292
          301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
              Db
          293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 352
Qу
          361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              Db
          353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N; Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or
dEGF; MGF-b; milk growth factor b; TGF-type II
C; Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence revision 28-Feb-1992 #text change 16-Jul-1999
C; Accession: A40057; A42320; A05284; A24322; B61439
R; Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker,
C.C.
Mol. Endocrinol. 1, 693-698, 1987
A; Title: Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-betal.
A; Reference number: A40057; MUID: 91042552; PMID: 3153459
A; Accession: A40057
A; Molecule type: mRNA
A; Residues: 1-315 < VAN>
A; Cross-references: GB: M36271; NID: q163747; PIDN: AAA30778.1; PID: q163748
R; Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A; Title: Purification and characterization of transforming growth factor-beta2.3
and -beta1.2 heterodimers from bovine bone.
A; Reference number: A42320; MUID: 92129307; PMID: 1733936
A; Accession: A42320
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217 < OGA>
R; Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan,
Y.C.E.; Stein, S.; Lehrman, S.R.; Smith, J.M.; Lamb, L.C.; Sporn, M.B.
Biochemistry 22, 5692-5698, 1983
A; Title: Purification and properties of a type beta transforming growth factor
from bovine kidney.
A; Reference number: A05284; MUID: 84104793; PMID: 6607069
A; Accession: A05284
A; Molecule type: protein
A; Residues: 204-218 < ROB>
R; Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti,
A.; Siegel, N.R.; Galluppi, G.R.; Piez, K.A.
J. Biol. Chem. 261, 5693-5695, 1986
A; Title: Cartilage-inducing factor-A. Apparent identity to transforming growth
factor-beta.
A; Reference number: A24322; MUID: 86195954; PMID: 3754555
A; Accession: A24322
A; Molecule type: protein
A; Residues: 204-233 <SEY>
R; Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
```

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A; Title: Separation, purification, and sequence identification of TGF-betal and
TGF-beta2 from bovine milk.
A; Reference number: A61439; MUID: 92189724; PMID: 1799413
A; Accession: B61439
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>
C; Comment: This polypeptide is composed of two polypeptide chains cross-linked
by disulfide bonds. It has been found in neoplastic and non-neoplastic tissues.
C; Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic
mitogenic activity, but in soft agar, it reacts synergistically with either type
I TFG or EGF, and induces cell proliferation. Cells grown in monolayer do not
respond in a similar manner to these growth factors, but morphologically do
acquire a transformed phenotype.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Ouery Match
                       74.6%; Score 1577; DB 2; Length 315;
 Best Local Similarity
                       91.3%; Pred. No. 6.3e-119;
 Matches 295; Conservative
                             9; Mismatches
                                           11;
                                                Indels
                                                         8; Gaps
                                                                    1:
          76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
Qу
            1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
Dh
Qу
         136 NTSELREAVPEPVLLSRAELRLKLKLKVEOHVELYOKYSNDSWRYLSNRLLAPSDSPEW 195
            61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
Db
         196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            Db
         121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
         256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
            Db
         181 PFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
         316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
QУ
            Db
         233 WKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALEPLPIV 292
         376 YYVGRKPKVEOLSNMIVRSCKCS 398
Qу
             Db
         293 YYVGRKPKVEOLSNMIVRSCKCS 315
RESULT 10
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N; Alternate names: TGF-beta 4
C; Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C; Accession: A41918; A34941; S03110
R; Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
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A; Title: Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA.
A; Reference number: A41918; MUID: 92357039; PMID: 1353860
A; Accession: A41918
A; Molecule type: mRNA
A; Residues: 1-373 <BUR>
A; Cross-references: GB: M31160; GB: X08012; GB: S41706; NID: g1262437;
PIDN:AAB05637.1; PID:g1262438
A; Note: sequence extracted from NCBI backbone (NCBIN:110186, NCBIP:110187)
A; Note: this report corrects and reinterprets the sequence from reference A34941
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic
acid encoding transforming growth factor beta-4 from chicken embryo
chondrocytes.
A; Reference number: A34941; MUID: 89112198; PMID: 2464131
A; Accession: A34941
A; Molecule type: mRNA
A; Residues: 'MDPMSIGPKSCGGSPWRPPGTAPWSIGSRRATASSSCSTSSRVRAEVGGRAL', 122-
209, 'D', 211-373 <JAK>
A; Cross-references: EMBL: X08012
A; Note: this sequence has been corrected in A41918
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor
F;1/Domain: signal sequence (fragment) #status predicted <SIG>
F;223-225/Region: cell attachment (R-G-D) motif
F;260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F;54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match
                       50.1%; Score 1059.5; DB 2; Length 373;
 Best Local Similarity 54.5%; Pred. No. 2.7e-77;
 Matches 208; Conservative 52; Mismatches 99; Indels
                                                         23; Gaps
                                                                     8;
          30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
          90 GES-VEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
              Db
         62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWOPOSHSIFFVFNVSRARRG-GRPT 120
         149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
            Db
         121 LLHRAELRMLROKAAADSAGTEORLELYOGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
         204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            1 111: 1: 1:11 1 :
                                        :: 1 11
                                                : [ ] [ : ]
Db
         181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239
         259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316
Qу
             Db
         240 LAMALPAERANELHSARRRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLQW 291
         317 KWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVY 376
QУ
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292 KWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDPLPIIY 351

Db

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377 YVGRKPKVEQLSNMIVRSCKCS 398
Оv
              Db
          352 YVGRNVRVEQLSNMVVRACKCS 373
RESULT 11
A34939
transforming growth factor beta-3 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 16-Jul-1999
C; Accession: A34939; S25850; S36125; S36124; I51181
R; Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 747-755, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a novel transforming
growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes.
A; Reference number: A34939; MUID: 89096966; PMID: 3211158
A; Accession: A34939
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-412 < JAK>
A; Cross-references: GB: M31154; NID: q212758; PIDN: AAA49089.1; PID: q212759
R; Burt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A; Title: Comparative analysis of human and chicken transforming growth factor-
beta-2 and -beta-3 promoters.
A; Reference number: S25850; MUID: 92134496; PMID: 1840616
A; Accession: S25850
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <BUR>
A; Cross-references: EMBL: X58127; NID: g63815; PIDN: CAA41128.1; PID: g63816
A; Accession: S36125
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 119-172 < BU2>
A; Cross-references: EMBL: X60055; NID: g396688; PIDN: CAA42653.1; PID: g396689
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
A; Accession: S36124
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 173-322, 'ELPT', 327-412 < BU3>
A; Cross-references: EMBL: X60091
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
1991
R; Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.;
Cubert, J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 6, 1285-1298, 1992
A; Title: Identification and characterization of the chicken transforming growth
factor-beta 3 promoter.
A; Reference number: I51181; MUID: 93024487; PMID: 1406706
A; Accession: I51181
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <JA2>
A;Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173
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C; Genetics:

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A; Introns: 216/1; 252/1; 309/2; 360/3
A; Note: list of introns may be incomplete
C; Superfamily: inhibin
C; Keywords: qlycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
F;74,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       41.4%; Score 876; DB 2; Length 412;
 Query Match
 Best Local Similarity 47.1%; Pred. No. 1.7e-62;
 Matches 198; Conservative 56; Mismatches 114; Indels 52; Gaps
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         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
                    1: | :|:
Db
          9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNOIYDKF 124
Qу
              |::
         67 YOILALYNSTRELL--EEMEEEKEESCSOENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
Db
         125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
Qу
                                 : || :||:|
         125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEORIELFOILRPDEHI 180
Dh
         178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
Qу
               181 AKORYLSGRNVOTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240
Db
         230 N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
Qу
                :: | :|
                             241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300
Db
         279 DYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIW 338
Qу
                   301 -----ALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYFANFCSGPCPYLR 352
Db
         339 SLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 SADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
Db
RESULT 12
B61036
transforming growth factor beta-5 precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence revision 03-Feb-1994 #text change 16-Jul-1999
C; Accession: A34929; B61036
R; Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn,
M.B.; Melton, D.A.
J. Biol. Chem. 265, 1089-1093, 1990
A; Title: Identification of a novel transforming growth factor-beta (TGF-beta5)
mRNA in Xenopus laevis.
A; Reference number: A34929; MUID: 90110090; PMID: 2295601
A; Accession: A34929
A; Molecule type: mRNA
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A; Residues: 1-382 < KON>

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A; Cross-references: GB: J05180; NID: g214821; PIDN: AAA49968.1; PID: g214822
R; Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert,
M.L.; Kondaiah, P.; Danielpour, D.; Kehrl, J.H.; Wahl, S.M.; Dawid, I.B.; Sporn,
M.B.
Growth Factors 2, 135-147, 1990
A; Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium
conditioned by Xenopus XTC cells.
A; Reference number: A61036; MUID: 90253806; PMID: 2340184
A; Accession: B61036
A; Molecule type: protein
A; Residues: 271-276, 'X', 278-284, 'XX', 287-299 < ROB>
C; Superfamily: inhibin
C; Keywords: growth factor
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>
                       41.3%; Score 873; DB 2; Length 382;
 Best Local Similarity 46.9%; Pred. No. 2.6e-62;
 Matches 190; Conservative 55; Mismatches 122; Indels 38; Gaps
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           9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGDV 68
Qу
                           : : | | | | | | | |
           1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGOILSKLKLDKTPDV-DS 59
Db
          69 PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNOIYDK 123
Qу
                : [[[[]:[
                                                           | | | :: |
          60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
Db
         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEOHVELYOKYSNDSW-- 179
Qу
                       ::|:||: || :
         116 ----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTTH 170
Db
         180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
Qу
                         | | | | | | |
                                                       : :||
         171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
Db
         236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYC 293
Qу
             | ||
                    1111::
                               :|:|:: | | |
                                             : ||| :|
         227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR------GVGQEYC 277
Db
         294 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 353
Qу
             278 FGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVLSLYNQ 337
Db
         354 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
             Db
         338 NNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382
RESULT 13
S01825
transforming growth factor beta-3 precursor - pig
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text change 16-Jul-1999
C; Accession: S01825
R; Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee,
L.; Mason, A.J.; Miller, D.A.; Coffey, R.J.; Moses, H.L.; Chen, E.Y.
EMBO J. 7, 3737-3743, 1988
```

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A; Title: A new type of transforming growth factor-beta, TGF-beta3.
A; Reference number: S01824; MUID: 89091120; PMID: 3208746
A; Accession: S01825
A; Molecule type: mRNA
A; Residues: 1-409 < DER >
A; Cross-references: EMBL: X14150; NID: g2127; PIDN: CAA32363.1; PID: g2128
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-297/Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>
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                      39.7%; Score 838.5; DB 2; Length 409;
 Best Local Similarity 45.6%; Pred. No. 1.7e-59;
 Matches 190; Conservative 58; Mismatches 122; Indels 47; Gaps
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         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
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                     Db
          7 LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGOILSKLRLTSPPDPSML--ANIP 64
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNOIYDKFKG 126
Qу
              Db
         65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
QУ
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEOHVELYOKYSND----S 178
                               :: || | : :
        125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Db
Qу
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
             Db
        181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
Qу
        231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRDYK 281
              241 QEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAQRKKR--- 297
Db
        282 DDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD 341
Qу
                Db
        298 ----ALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSAD 352
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        353 TTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVVKSCKCS 409
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transforming growth factor beta-3 precursor - mouse
C; Species: Mus musculus (house mouse)
C;Date: 03-Apr-1992 #sequence revision 03-Apr-1992 #text change 16-Jul-1999
C; Accession: A41397; A61039; A61225
R; Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A; Title: Complementary DNA cloning of the murine transforming growth factor-
beta3 (TGFbeta3) precursor and the comparative expression of TGFbeta3 and
TGFbetal messenger RNA in murine embryos and adult tissues.
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A; Reference number: A41397; MUID: 90190650; PMID: 2628730

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A; Accession: A41397
A; Molecule type: mRNA
A; Residues: 1-410 <MIL>
A; Cross-references: GB: M32745; NID: g201949; PIDN: AAA40422.1; PID: q201950
R; Denhez, F.; Lafyatis, R.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Growth Factors 3, 139-146, 1990
A; Title: Cloning by polymerase chain reaction of a new mouse TGF-beta, mTGF-
beta3.
A; Reference number: A61039; MUID: 91000714; PMID: 2206556
A; Accession: A61039
A; Molecule type: mRNA
A; Residues: 1-410 < DEN>
R; Watrin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.
Cell Growth Differ. 2, 77-83, 1991
A; Title: Cell lineage specificity of expression of the murine transforming
growth factor beta-3 and transforming growth factor beta-1 genes.
A; Reference number: A61225; MUID: 91299576; PMID: 2069871
A; Accession: A61225
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 285-410 <WAT>
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-298/Domain: propeptide #status predicted <PRO>
F;259-261/Region: cell attachment (R-G-D) motif
F;299-410/Product: transforming growth factor beta-3 #status predicted <MAT>
F;72,133,140/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Qу
               1::
Db
          65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                 :: || | : :
                                   | | | | | | | | | |
                                                  : || :||:|
Db
         125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
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                        -: ||||||||
              Db
         181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240
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Qу
                              : | |:|| |
                : :: | ::
Db
         241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK---- 296
         283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
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RESULT 15
A55706
transforming growth factor beta-3 precursor - rat
C; Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1995 #sequence revision 03-Mar-1995 #text change 16-Jul-1999
C; Accession: A55706; B40699; S36042
R; Wang, J.; Kuliszewski, M.; Yee, W.; Sedlackova, L.; Xu, J.; Tseu, I.; Post, M.
J. Biol. Chem. 270, 2722-2728, 1995
A; Title: Cloning and expression of glucocorticoid-induced genes in fetal rat
lung fibroblasts. Transforming growth factor-beta-3.
A; Reference number: A55706; MUID: 95155340; PMID: 7852342
A; Accession: A55706
A; Molecule type: mRNA
A; Residues: 1-410 <WAN>
A; Cross-references: GB: U03491
A; Note: it is uncertain whether Met-1 is the initiator
R; McKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M.
J. Cell Biol. 121, 1397-1407, 1993
A; Title: A role for TGF-beta in oligodendrocyte differentiation.
A; Reference number: A40699; MUID: 93286190; PMID: 8509457
A; Accession: B40699
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 157-211 < MCK>
A; Cross-references: EMBL: X71903; NID: g311326; PIDN: CAA50722.1; PID: g311327
C; Superfamily: inhibin
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 Query Match
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Qу
              |::
Db
          65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                :: || | : :
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Qу
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Db
Qу
         231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
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283 DDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342

Qу

Search completed: October 28, 2003, 09:09:47

Job time : 15.1517 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:08:41; Search time 7.97725 Seconds

(without alignments)

2346.251 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41:\*

ᇰ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	guery Match	Length	DB	ID	Description
				<b></b>		zeseripeion
1	2035	96.3	390	1	TGF1_PIG	P07200 sus scrofa
2	1934	91.5	390	1	TGF1_SHEEP	P50414 ovis aries
3	1921	90.9	390	1	TGF1 HUMAN	P01137 homo sapien
4	1919	90.8	390	1	TGF1 CERAE	P09533 cercopithec
5	1898	89.8	390	1	TGF1 CANFA	P54831 canis famil
6	1844	87.2	390	1	TGF1 HORSE	019011 equus cabal
7	1840	87.0	390	1	TGF1_MOUSE	P04202 mus musculu

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8 1840 87.0 390 1 TGF1_RAT P17246 rattus norv 9 1831 86.6 390 1 TGF1_CAVPO O921y6 cavia porce 10 1577 74.6 3155 1 TGF1_BOVIN P18341 bos taurus 11 1059.5 50.1 373 1 TGF1_CHICK P09531 gallus gall 12 873 41.3 382 1 TGF1_CHICK P16176 xenopus lae 13 857 40.5 412 1 TGF3_CHICK P16176 xenopus lae 14 838.5 39.7 409 1 TGF3_CHICK P16176 xenopus lae 15 835 39.5 410 1 TGF3_MOUSE P17125 mus musculu 16 834 39.5 412 1 TGF3_RAT Q07258 rattus norv 17 832 39.4 412 1 TGF3_HUMAN P10600 homo sapien 18 831.5 39.3 414 1 TGF2_MOUSE P27090 mus musculu 18 831.5 39.3 414 1 TGF2_MOUSE P27090 mus musculu 19 816.5 38.6 414 1 TGF2_CHICK P30317 gallus gall 22 812.5 38.4 435 1 TGF2_CHICK P30317 gallus gall 22 812.5 38.4 442 1 TGF2_FIG P09858 sus scrofa 23 812.5 38.4 442 1 TGF2_FIG P09858 sus scrofa 23 812.5 38.4 442 1 TGF2_FIG P09858 sus scrofa 24 482 22.8 112 1 TGF2_BOVIN P21214 bos taurus 25 339 16.0 375 1 GDF8_MELGA O42221 meleagris g 26 337 15.9 375 1 GDF8_PIG O18831 sus scrofa 28 326 15.4 375 1 GDF8_PIG O18831 sus scrofa 29 324 15.3 376 1 GDF8_PIG O18831 sus scrofa 29 324 15.3 376 1 GDF8_PAPHA O18828 papio hamad 29 324 15.3 376 1 GDF8_RAT O35312 rattus norv 34 303.5 14.4 405 1 GDF8_BANA O14793 homo sapien 31 322 15.2 376 1 GDF8_BANA O14793 homo sapien 34 303.5 14.4 405 1 GDF8_BANA O14793 homo sapien 34 303.5 14.4 405 1 GDF8_BANA O14793 homo sapien 34 303.5 14.4 405 1 GDF8_BANA O14793 homo sapien 36 291 13.8 374 1 GDF8_BANA O15793 homo sapien 37 282 13.3 345 1 GDF8_BANA O15793 homo sapien 38 281.5 13.3 425 1 HBA_BANE O4222 brachydanio 278 13.1 424 1 HBA_BANE O4222 brachydanio 278 13.1 425 1 HBA_BANE O4222 brachydanio 278 13.1 426 1 HBA_BANE O4222 brachydanio 278 13.1 42
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## ALIGNMENTS

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RESULT 1
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AC
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DT
    01-APR-1988 (Rel. 07, Created)
DT
     01-APR-1988 (Rel. 07, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
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    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
     Sus scrofa (Pig).
OS
OC
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OC
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OX
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RN
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     TISSUE=Ovary;
     MEDLINE=87174844; PubMed=3470708;
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RA
     Derynck R., Rhee L.;
RT
     "Sequence of the porcine transforming growth factor-beta precursor.";
RL
     Nucleic Acids Res. 15:3187-3187(1987).
RN
RP
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RC
     STRAIN=Miniature swine;
RX
     MEDLINE=89054010; PubMed=2461367;
     Kondaiah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RA
     Sporn M.B., Roberts A.B.;
RA
     "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT
RT
     Evidence for alternate splicing and polyadenylation.";
     J. Biol. Chem. 263:18313-18317(1988).
RL
RN
     [3]
RP
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RX
     MEDLINE=88335639; PubMed=3166520;
RA
     Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
     "Nucleotide sequence of chicken transforming growth factor-beta 1
RT
     (TGF-beta 1).";
RT
RL
     Nucleic Acids Res. 16:8730-8730(1988).
RN
RP
     SHOWS THAT REF.3 SEQUENCE IS FROM PIG.
RA
     Jakowlew S.B.;
     Unpublished observations (MAR-1996).
RL
RN
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RP
RA
     Wimmers K., Chomdej S., Ponsuksili S., Schellander K.;
     "Polymorphism in the porcine transforming growth factor beta 1
RT
RT
     gene.";
RL
     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN
     [6]
     SEOUENCE OF 279-322.
RΡ
     MEDLINE=87102890; PubMed=2879635;
RX
     Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA
     Lucas R., Massague J.;
RA
     "The transforming growth factor-beta system, a complex pattern of
RT
     cross-reactive ligands and receptors.";
RT
     Cell 48:409-415(1987).
RL
     -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
CC
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
         HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
         ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
CC
         A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: Homodimer; disulfide-linked.
CC
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CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
     -!- CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
CC
CC
         WHITE LEGHORN, SEEMS (REF.4) TO ORIGINATE FROM PIG.
     ______
CC
CC
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     between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    or send an email to license@isb-sib.ch).
CC
    ______
DR
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    EMBL; M23703; AAA64616.1; -.
    EMBL; X12373; CAA30933.1; -.
DR
DR
    EMBL; AF461808; AAL57902.1; -.
    PIR; A27512; A27512.
DR
    HSSP; P01137; 1KLA.
DR
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    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
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    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal; Polymorphism.
FT
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                      23
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                24
FT
    PROPEP
                      278
FT
              279
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                              TRANSFORMING GROWTH FACTOR BETA 1.
FΤ
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                     294
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    DISULFID 293
                              BY SIMILARITY.
FT
                     356
                             BY SIMILARITY.
FT
    DISULFID 322
                     387
    DISULFID 326 389 BY SIMILARITY.

DISULFID 355 355 INTERCHAIN (BY SIMILARITY).

CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
    DISULFID 326 389
DISULFID 355 355
CARBOHYD 82 82
FT
FT
FT
FT
FT
FT
    SITE
              244
                     246
                              CELL ATTACHMENT SITE (POTENTIAL).
    VARIANT
FT
              114
                     114
                              L -> V.
    CONFLICT
FT
               6
                      7
                              LR \rightarrow PG (IN REF. 3).
    CONFLICT
              180
FT
                      180
                              R \rightarrow G (IN REF. 3).
FT
    CONFLICT
               237
                     237
                              N \rightarrow NA (IN REF. 3).
SQ
    SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;
 Query Match
                        96.3%; Score 2035; DB 1; Length 390;
 Best Local Similarity 97.0%; Pred. No. 9e-154;
 Matches 386; Conservative 1; Mismatches 3; Indels 8; Gaps
Qу
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QУ
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
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Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
             Db
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Db
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             Db
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QУ
             Db
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Qу
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Db
RESULT 2
TGF1 SHEEP
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ΙD
                  STANDARD;
                                 PRT; 390 AA.
AC
    P50414;
DT
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DΕ
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Ovis aries (Sheep).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Caprinae; Ovis.
OX
    NCBI TaxID=9940;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=95121932; PubMed=7821809;
    Woodall C.J., McLaren L.J., Watt N.J.;
RA
RT
     "Sequence and chromosomal localisation of the gene encoding ovine
RT
    latent transforming growth factor-beta 1.";
RL
    Gene 150:371-373(1994).
RN
     [2]
RP
    SEQUENCE OF 281-390 FROM N.A.
RC
    STRAIN=Merino; TISSUE=Skin;
RX
    MEDLINE=95268698; PubMed=7749621;
RA
    Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RT
     "Growth factor expression in skin during wool follicle development.";
RL
    Comp. Biochem. Physiol. 110B:697-705(1995).
CC
     -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
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CC
CC
    use by non-profit institutions as long as its content is in no way
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    or send an email to license@isb-sib.ch).
    CC
DR
    EMBL; X76916; CAA54242.1; -.
DR
    EMBL; L36038; AAA31526.1; -.
    PIR; I46463; I46463.
DR
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
               1
                    23
                            POTENTIAL.
                    278
FT
    PROPEP
              24
                             POTENTIAL.
FT
    CHAIN
              279
                    390
                             TRANSFORMING GROWTH FACTOR BETA 1.
             285
FT
    DISULFID
                    294
                            BY SIMILARITY.
    DISULFID 293
FΤ
                   356
                            BY SIMILARITY.
FT
    DISULFID 322
                   387
                            BY SIMILARITY.
FT
    DISULFID 326
                   389
                            BY SIMILARITY.
FT
    DISULFID
             355
                   355
                            INTERCHAIN (BY SIMILARITY).
FT
                    82
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              82
FT
    CARBOHYD
              136
                    136
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FΤ
    CARBOHYD
             176
                    176
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                   246
FT
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             244
                           CELL ATTACHMENT SITE (POTENTIAL).
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                      91.5%; Score 1934; DB 1; Length 390;
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 Best Local Similarity 91.7%; Pred. No. 9e-146;
 Matches 365; Conservative 10; Mismatches 15; Indels
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         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
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Qу
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Db
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Qу
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Db
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Qу
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QУ
          361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              Db
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RESULT 3
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ΙD
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AC
     P01137; Q9UCG4;
DT
     21-JUL-1986 (Rel. 01, Created)
     01-FEB-1991 (Rel. 17, Last sequence update)
DT
DT
     15-SEP-2003 (Rel. 42, Last annotation update)
DE
     Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
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OS
     Homo sapiens (Human).
OC
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OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
     NCBI TaxID=9606;
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RX
    MEDLINE=87174845; PubMed=3470709;
RA
     Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
RT
     "Intron-exon structure of the human transforming growth factor-beta
RT
     precursor gene.";
RL
    Nucleic Acids Res. 15:3188-3189(1987).
RN
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=85296301; PubMed=3861940;
RA
    Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
RA
    Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RT
     "Human transforming growth factor-beta complementary DNA sequence and
RT
     expression in normal and transformed cells.";
    Nature 316:701-705(1985).
RL
RN
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RΡ
    SEQUENCE FROM N.A.
RC
    TISSUE=Duodenum, and Eve:
RX
    MEDLINE=22388257; PubMed=12477932;
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    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
RA
    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
RA
    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA
    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA
     Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT
     "Generation and initial analysis of more than 15,000 full-length
     human and mouse cDNA sequences.";
RT
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
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RΡ
     SEQUENCE OF 279-390 FROM N.A.
RC
     TISSUE=Carcinoma;
RA
     Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RA
     Urushizaki I., Takahashi Y., Ito H.;
RT
     "Cloning and expression of the gene for human transforming growth
RT
     factor-beta in Escherichia coli.";
RL
     Tumor Res. 22:41-55(1987).
RN
     [5]
     SEQUENCE OF 279-329.
RΡ
RC
     TISSUE=Bladder carcinoma;
RX
     MEDLINE=93229900; PubMed=8471846;
RA
     Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
RA
     Hu S., Westcott K.R.;
     "Recombinant human transforming growth factor-beta 1: expression by
RT
RT
     Chinese hamster ovary cells, isolation, and characterization.";
     Protein Expr. Purif. 4:130-140(1993).
RL
RN
RP
     SEQUENCE OF 279-301.
     MEDLINE=85131019; PubMed=2982829;
RX
RA
     Massague J., Like B.;
     "Cellular receptors for type beta transforming growth factor. Ligand
RT
     binding and affinity labeling in human and rodent cell lines.";
RT
RL
     J. Biol. Chem. 260:2636-2645(1985).
RN
     [7]
RP
     STRUCTURE BY NMR OF 279-390.
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     MEDLINE=93144319; PubMed=8424942;
RA
     Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
     Torchia D.A.;
RA
     "Transforming growth factor beta 1: NMR signal assignments of the
RT
RT
     recombinant protein expressed and isotopically enriched using Chinese
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RT
RL
     Biochemistry 32:1152-1163(1993).
RN
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RP
RX
     MEDLINE=93144320; PubMed=8424943;
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RA
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
     Torchia D.A.;
RT
     "Transforming growth factor beta 1: secondary structure as determined
RT
     by heteronuclear magnetic resonance spectroscopy.";
RL
     Biochemistry 32:1164-1171(1993).
RN
     [9]
RP
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RX
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RA
     Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
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RT
     "Transforming growth factor beta 1: three-dimensional structure in
RT
     solution and comparison with the X-ray structure of transforming
RT
     growth factor beta 2.";
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RL
    Biochemistry 35:8517-8534(1996).
CC
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
        CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
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    the European Bioinformatics Institute. There are no restrictions on its
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    use by non-profit institutions as long as its content is in no way
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    modified and this statement is not removed. Usage by and for commercial
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    or send an email to license@isb-sib.ch).
CC
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DR
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    EMBL; X05840; CAA29283.1; JOINED.
DR
    EMBL; X05843; CAA29283.1; JOINED.
DR
    EMBL; X05844; CAA29283.1; JOINED.
DR
DR
    EMBL; X05849; CAA29283.1; JOINED.
DR
    EMBL; X05850; CAA29283.1; JOINED.
DR
    EMBL; X02812; CAA26580.1; ALT SEQ.
DR
    EMBL; BC001180; AAH01180.1; -.
DR
    EMBL; BC000125; AAH00125.1; -.
    EMBL; BC022242; AAH22242.1; -.
DR
DR
    EMBL; M38449; AAA36735.1; -.
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DR
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DR
DR
    Genew; HGNC:11766; TGFB1.
    MIM; 190180; -.
DR
DR
    GO; GO:0006916; P:anti-apoptosis; TAS.
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DR
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
FT
    SIGNAL
                      23
                               POTENTIAL.
                1
FT
    PROPEP
                      278
                24
FT
                279
                      390
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    CHAIN
FT
    DISULFID
               285
                      294
    DISULFID 293
FT
                      356
FT
    DISULFID 322
                      387
FT
    DISULFID
               326
                      389
FT
    DISULFID 355
                     355
                              INTERCHAIN.
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FT
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                    82
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                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              136
                    136
FT
    CARBOHYD
              176
                    176
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
                            CELL ATTACHMENT SITE (POTENTIAL).
    SITE
              244
                    246
FT
    CONFLICT
              10
                    10
                            L \rightarrow P (IN REF. 2).
                            R \rightarrow RR (IN REF. 2).
FT
    CONFLICT
              159
                    159
FT
    STRAND
              281
                    281
FT
    TURN
              282
                    287
FT
    STRAND
              294
                    296
FT
    STRAND
              300
                    300
FT
    TURN
              302
                    305
FT
    STRAND
              313
                    313
FT
    STRAND
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    HELIX
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                    346
FT
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FT
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FT
    STRAND
              373
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SQ
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 Best Local Similarity
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            Db
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Qу
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Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
Db
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Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 4
TGF1 CERAE
    TGF1 CERAE
                STANDARD;
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                                   390 AA.
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AC
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    01-MAR-1989 (Rel. 10, Created)
DT
DT
    01-MAR-1989 (Rel. 10, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
    Cercopithecus aethiops (Green monkey) (Grivet).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC
OC
    Cercopithecinae; Cercopithecus.
ΟX
    NCBI TaxID=9534;
RN
    [1]
RР
    SEQUENCE FROM N.A.
RX
    MEDLINE=87246074; PubMed=3474130;
RA
    Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
    "Cloning and sequence analysis of simian transforming growth
RT
RT
    factor-beta cDNA.";
RL
    DNA 6:239-244(1987).
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION,
CC
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
        CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    _____
CC
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CC
    or send an email to license@isb-sib.ch).
CC
    ______
    EMBL; M16658; AAA35369.1; -.
DR
    PIR; A26960; A26960.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
               1
                      16
                              POTENTIAL.
                17
                      278
FT
    PROPEP
                     390
                               TRANSFORMING GROWTH FACTOR BETA 1.
FT
               279
    CHAIN
    DISULFID 285 294
                              BY SIMILARITY.
FT
    DISULFID 293
                     356
                              BY SIMILARITY.
FT
    DISULFID 322 387
                              BY SIMILARITY.
FT
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FT
                    355
                            INTERCHAIN (BY SIMILARITY).
    DISULFID
              355
FT
              82
                    82
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
    CARBOHYD
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              136
                    136
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                    176
                            CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
              244
                    246
             390 AA; 44356 MW; DFF63E2BAB44320E CRC64;
SO
    SEQUENCE
 Query Match
                     90.8%; Score 1919; DB 1; Length 390;
                     91.5%; Pred. No. 1.4e-144;
 Best Local Similarity
                                                      8;
 Matches 364; Conservative 10; Mismatches
                                         16; Indels
                                                          Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
QУ
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
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QУ
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Db
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Qу
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Db
        361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 5
TGF1 CANFA
ID
    TGF1 CANFA
                STANDARD;
                             PRT;
                                   390 AA.
    P54831;
AC
DT
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
DТ
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
    TGFB1.
GN
OS
    Canis familiaris (Dog).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
    NCBI TaxID=9615;
OX
RN
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=Jugular vein endothelial;
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BY SIMILARITY.

FT

DISULFID

326

389

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RX
    MEDLINE=95237630; PubMed=7721110;
RA
    Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;
RT
    "Cloning of a canine cDNA homologous to the human transforming growth
RT
    factor-beta 1-encoding gene.";
RL
    Gene 155:307-308(1995).
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
    _____
CC
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    or send an email to license@isb-sib.ch).
    _____
CC
DR
    EMBL; L34956; AAA51458.1; -.
DR
    PIR; JC4023; JC4023.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
                1
FT
                     23
                              POTENTIAL.
    SIGNAL
                      278
                               BY SIMILARITY.
FΤ
    PROPEP
                24
                     390
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    CHAIN
               279
FT
    DISULFID
                     294
                              BY SIMILARITY.
              285
              293
                              BY SIMILARITY.
FT
                     356
    DISULFID
                              BY SIMILARITY.
               322
                     387
FT
    DISULFID
                     389
                              BY SIMILARITY.
FT
              326
    DISULFID
FT
              355
                    355
                              INTERCHAIN.
    DISULFID
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               82
                      82
FT
    CARBOHYD
              136
                     136
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                     176
                              CELL ATTACHMENT SITE (POTENTIAL).
FT
                     246
    SITE
               244
SQ
    SEQUENCE 390 AA; 44185 MW; EB4780E88B7B590E CRC64;
                       89.8%; Score 1898; DB 1; Length 390;
 Query Match
  Best Local Similarity 90.7%; Pred. No. 6.4e-143;
 Matches 361; Conservative 12; Mismatches 17; Indels
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         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
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         61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
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Qу
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Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
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Qу
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Db
QУ
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Db
        361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
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Db
RESULT 6
TGF1 HORSE
ΙD
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                STANDARD;
                             PRT:
                                   390 AA.
AC
    019011;
    15-JUL-1998 (Rel. 36, Created)
DT
    15-JUL-1998 (Rel. 36, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
GN
    TGFB1.
    Equus caballus (Horse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC
OX
    NCBI TaxID=9796;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Lymph node;
    MEDLINE=98185507; PubMed=9524819;
RX
    Penha-Goncalves M.N., Onions D.E., Nicolson L.;
RA
    "Cloning and sequencing of equine transforming growth factor-beta 1
RT
RT
    (TGF beta-1) cDNA.";
    DNA Seq. 7:375-378(1997).
RL
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
       PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
       TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
       HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
       ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
       A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
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CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
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    or send an email to license@isb-sib.ch).
    ______
CC
DR
    EMBL; X99438; CAA67801.1; -.
    HSSP; P01137; 1KLA.
DR
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
             1
                   23
FT
    SIGNAL
                            POTENTIAL.
FT
    PROPEP
              24
                    278
                            BY SIMILARITY.
FT
    CHAIN
              279
                   390
                           TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID 285 294
                           BY SIMILARITY.
   DISULFID 293 356
DISULFID 322 387
DISULFID 326 389
FT
                           BY SIMILARITY.
                           BY SIMILARITY.
FT
                           BY SIMILARITY.
FT
FТ
    DISULFID 355 355
                           INTERCHAIN (BY SIMILARITY).
FT
             82
                    82
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    CARBOHYD
FT
    CARBOHYD 136 136
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
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             176 176
    SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;
SQ
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Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
               Db
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        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGFRLSAHCSCDSKDNTLRVGINGFS 240
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Qу
         241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
             Db
         241 SSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRHRR------ALDTNYCFSSTEKN 292
Ov
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
             293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
QУ
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Dh
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RESULT 7
TGF1 MOUSE
ΙD
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    P042\overline{0}2;
AC
DT
    20-MAR-1987 (Rel. 04, Created)
DT
    20-MAR-1987 (Rel. 04, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC.
OX
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RN
    [1]
    SEQUENCE FROM N.A.
RP
RX
    MEDLINE=86168129; PubMed=3007454;
RA
    Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT
    "The murine transforming growth factor-beta precursor.";
RL
    J. Biol. Chem. 261:4377-4379(1986).
RN
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=BALB/c;
    MEDLINE=96096545; PubMed=8522200;
RX
RA
    Guron C., Sudarshan C., Raghow R.;
RT
    "Molecular organization of the gene encoding murine transforming
RT
    growth factor beta 1.";
RL
    Gene 165:325-326(1995).
RN
    [3]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
RA
    Poirot L., Benoist C., Mathis D.;
RT
    "Transforming growth factor-beta 1 sequence and expression: no
RT
    difference between NOD/Lt and C57Bl/6 mouse strains.";
RL
    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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    or send an email to license@isb-sib.ch).
CC
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    EMBL; M13177; AAA40423.1; -.
DR
DR
    EMBL; L42462; AAB00138.1; -.
DR
    EMBL; L42456; AAB00138.1; JOINED.
DR
    EMBL; L42457; AAB00138.1; JOINED.
DR
    EMBL; L42458; AAB00138.1; JOINED.
DR
    EMBL; L42459; AAB00138.1; JOINED.
DR
    EMBL; L42460; AAB00138.1; JOINED.
     EMBL; L42461; AAB00138.1; JOINED.
DR
     EMBL; AJ009862; CAA08900.1; -.
DR
DR
    PIR; A01396; WFMS2.
DR
    HSSP; P01137; 1KLA.
DR
    MGD; MGI:98725; Tgfb1.
DR
    GO; GO:0005578; C:extracellular matrix; IDA.
    GO; GO:0006954; P:inflammatory response; IMP.
DR
    GO; GO:0007515; P:lymph gland development; IMP.
DR
DR
    GO; GO:0008220; P:necrosis; IMP.
DR
    GO; GO:0016202; P:regulation of myogenesis; IDA.
DR
     InterPro; IPR002400; GF cysknot.
DR
     InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
     InterPro; IPR001111; TGFb N.
DR
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     Pfam; PF00688; TGFb propeptide; 1.
DR
     PRINTS; PR00438; GFCYSKNOT.
DR
     PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
                        23
    SIGNAL
                 1
                                 POTENTIAL.
    PROPEP
                 24
                       278
FT
                                 TRANSFORMING GROWTH FACTOR BETA 1.
FT
                279
                       390
    CHAIN
FT
    DISULFID
              285
                      294
                                BY SIMILARITY.
FT
    DISULFID
              293
                      356
                                BY SIMILARITY.
                                BY SIMILARITY.
FT
    DISULFID
               322
                      387
                                 BY SIMILARITY.
FT
    DISULFID
               326
                       389
                355
                       355
                                 INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
FT
    CARBOHYD
                82
                       82
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
                136
                       136
FT
    CARBOHYD
                176
                       176
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
                244
                       246
                                CELL ATTACHMENT SITE (POTENTIAL).
    SEQUENCE
               390 AA; 44310 MW; 4381A51B711D689E CRC64;
SQ
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                         87.0%; Score 1840; DB 1;
                                                     Length 390;
 Best Local Similarity
                         86.9%; Pred. No. 2.5e-138;
 Matches 346; Conservative 15; Mismatches 29; Indels
                                                                8; Gaps
                                                                            1:
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Db
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Qу
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
            Db
         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
QУ
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
            Db
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
Db
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
              241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
QУ
            Db
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 8
TGF1 RAT
    TGF1 RAT
                 STANDARD;
                              PRT;
                                    390 AA.
ΙD
AC
    P17246;
DT
    01-AUG-1990 (Rel. 15, Created)
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
    TGFB1.
GN
OS
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
    NCBI TaxID=10116;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Sprague-Dawley; TISSUE=Heart;
RX
    MEDLINE=90272425; PubMed=2349108;
RA
    Qian S.W., Kondaiah P., Roberts A.B., Sporn M.B.;
RT
    "cDNA cloning by PCR of rat transforming growth factor beta-1.";
RL
    Nucleic Acids Res. 18:3059-3059(1990).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
       HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
CC
       ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
       A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
```

```
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    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; X52498; CAA36741.1; -.
DR
    PIR; S10219; S10219.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                     23
                             POTENTIAL.
FT
    PROPEP
               24
                     278
FT
    CHAIN
               279
                     390
                             TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              285
                     294
                             BY SIMILARITY.
FT
              293
                    356
                             BY SIMILARITY.
    DISULFID
FT
    DISULFID
              322
                     387
                             BY SIMILARITY.
FT
    DISULFID
              326
                     389
                             BY SIMILARITY.
FT
    DISULFID
              355
                     355
                             INTERCHAIN (BY SIMILARITY).
FT
              82
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
                     82
FT
    CARBOHYD
              136
                     136
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                     176
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                             CELL ATTACHMENT SITE (POTENTIAL).
FΤ
              244
    SITE
                     246
    SEQUENCE
            390 AA; 44329 MW; 5E21108ED50D853C CRC64;
SQ
 Query Match
                       87.0%; Score 1840; DB 1; Length 390;
 Best Local Similarity
                      86.9%; Pred. No. 2.5e-138;
 Matches 346; Conservative 14; Mismatches
                                          30; Indels
                                                       8: Gaps
                                                                    1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Dh
```

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Qу
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
               111111111111
Db
         241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
QУ
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
             Db
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Qу
         361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
             Db
         353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
TGF1 CAVPO
ΙD
    TGF1 CAVPO
                   STANDARD;
                                 PRT;
                                        390 AA.
AC
    Q9Z1Y6; Q9QZB3; Q9R148;
DT
    16-OCT-2001 (Rel. 40, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Cavia porcellus (Guinea pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
    NCBI TaxID=10141;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Hartley;
RA
    Jeevan A., McMurray D.N., Yoshimura T.;
RT
    "Guinea pig transforming growth factor-beta in peritoneal exudates
RT
    after BCG vaccination.";
    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RL
RN
    SEQUENCE OF 265-382 FROM N.A.
RP
    MEDLINE=99144670; PubMed=10025978;
RX
    Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RA
RT
    "Spontaneous cytokine gene expression in normal guinea pig blood and
RT
    tissues.";
    Cytokine 10:851-859(1998).
RL
RN
RΡ
    SEQUENCE OF 279-371 FROM N.A.
    STRAIN=Hartley; TISSUE=Trachea;
RC
RA
    Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA
    Sekizawa K.:
RT
    "Guinea-pig transforming growth factor-beta expression in injured
RT
    tracheal epithelium.";
    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RL
CC
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
        CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
```

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CC
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    _____
DR
    EMBL; AF191297; AAF02780.1; -.
DR
    EMBL; AF097509; AAC83807.1; -.
DR
    EMBL; AF169347; AAD49347.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL 1 24
                             POTENTIAL.
FT
    PROPEP
               25
                     278
                              POTENTIAL.
FT
    CHAIN
              279 390
                             TRANSFORMING GROWTH FACTOR BETA 1.
                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
FT
    DISULFID 285
                    294
    DISULFID 293
DISULFID 322
FT
                   356
                    387
FT
                             BY SIMILARITY.
FT
    DISULFID 326 389
    DISULFID 355 355
FT
                             INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
               82
                     82
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 136 136
FT
    CARBOHYD 176 176
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
              244
                   246
                              CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
              279
FT
                   279
                             G \rightarrow P (IN REF. 3).
    CONFLICT
    CONFLICT 286 286
FT
                             F \rightarrow S (IN REF. 2).
FT
    CONFLICT
              309 309
                             K \rightarrow E (IN REF. 2).
FT
    CONFLICT
              322
                    322
                             C \rightarrow R (IN REF. 2).
FT
    CONFLICT
              350 350
                            A \rightarrow G (IN REF. 2).
SQ
    SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0FF1 CRC64;
                       86.6%; Score 1831; DB 1; Length 390;
 Query Match
 Best Local Similarity 86.7%; Pred. No. 1.3e-137;
 Matches 345; Conservative 15; Mismatches 30; Indels 8; Gaps
                                                                      1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSRLRLLPLLLPLLWLLVLAPGRPASGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
          61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEPDYYAKEVTRVLMVDNSHNI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
```

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Db
         121 YKSIETVAHSIYMFFNTSELREAVPDPLLLSRAELRMORLKLNVEOHVELYOKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNQLLTPSDTPEWLSFDVTGVVRQWLSQGEELEGFRFSAHCSCDSKDNTLRVEINGIG 240
Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
              Db
         241 PKRRGDLAAIHGMNRPFLLLMATPLERAQHLHSSRHRR-----GLDTNYCFSSTEKN 292
Qу
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
Qу
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Dh
         353 APCCVPQALEPLPIVYYVGRKAKVEQLSNMIVRSCKCS 390
RESULT 10
TGF1 BOVIN
ID
    TGF1 BOVIN
                  STANDARD;
                               PRT:
                                     315 AA.
    P18341;
AC
DT
    01-NOV-1990 (Rel. 16, Created)
    01-NOV-1990 (Rel. 16, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
DE
GN
    TGFB1.
OS
    Bos taurus (Bovine).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Bovinae; Bos.
OX
    NCBI TaxID=9913;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RX
    MEDLINE=91042552; PubMed=3153459;
    van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
RA
RA
    Baker C.C.;
    "Complementary deoxyribonucleic acid cloning of bovine transforming
RT
    growth factor-beta 1.";
    Mol. Endocrinol. 1:693-698(1987).
RT.
    [2]
RN
RP
    SUBUNITS.
RC
    TISSUE=Bone;
    MEDLINE=92129307; PubMed=1733936;
RX
RA
    Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RT
    "Purification and characterization of transforming growth factor-beta
    2.3 and -beta 1.2 heterodimers from bovine bone.";
RT
    J. Biol. Chem. 267:2325-2328(1992).
RL
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
CC
    -!- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2
```

```
CC
       have been found in bone.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
    ______
CC
CC
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    ______
CC
DR
    EMBL; M36271; AAA30778.1; -.
DR
    PIR; A40057; A40057.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
FT
    NON TER
               1
FΤ
    PROPEP
                    203
               <1
FT
    CHAIN
              204
                    315
                             TRANSFORMING GROWTH FACTOR BETA 1.
             210
FT
    DISULFID
                    219
                             BY SIMILARITY.
FT
    DISULFID 218
                  281
                            BY SIMILARITY.
FT
    DISULFID 247
                   312
                            BY SIMILARITY.
FT
    DISULFID 251
                   314
                            BY SIMILARITY.
FT
    DISULFID
              280
                    280
                             INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
               7
                     7
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
              61
                    61
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              101
                    101
                   171
FT
    SITE
              169
                            CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE 315 AA; 36269 MW; C2717A23D994E00E CRC64;
 Query Match
                      74.6%; Score 1577; DB 1; Length 315;
 Best Local Similarity 91.3%; Pred. No. 1.3e-117;
 Matches 295; Conservative 9; Mismatches 11; Indels
                                                     8; Gaps
0y
         76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
            Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
Qу
        136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
            Db
         61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
Qу
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
            Db
        121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
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Qу
         256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
             111111
                                         Db
         181 PFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
         316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
             Db
         233 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 292
QУ
         376 YYVGRKPKVEOLSNMIVRSCKCS 398
             Db
         293 YYVGRKPKVEQLSNMIVRSCKCS 315
RESULT 11
TGF1 CHICK
ΙD
    TGF1 CHICK STANDARD; PRT; 373 AA.
AC
    P09531;
DT
    01-MAR-1989 (Rel. 10, Created)
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
DE
    (Fragment).
GN
    TGFB1.
OS
    Gallus gallus (Chicken).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
    Gallus.
OX
    NCBI TaxID=9031;
RN
    [1]
RР
    SEQUENCE FROM N.A.
RC
    STRAIN=White leghorn;
RX
    MEDLINE=89112198; PubMed=2464131;
RA
    Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT
    "Complementary deoxyribonucleic acid cloning of a messenger
    ribonucleic acid encoding transforming growth factor beta 4 from
RT
    chicken embryo chondrocytes.";
RT
    Mol. Endocrinol. 2:1186-1195(1988).
RL
RN
    [2]
RP
    REVISIONS.
    MEDLINE=92357039; PubMed=1353860;
RX
    Burt D.W., Jakowlew S.B.;
RA
RT
    "Correction: a new interpretation of a chicken transforming growth
RT
    factor-beta 4 complementary DNA.";
RL
    Mol. Endocrinol. 6:989-992(1992).
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
CC
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CC
    DR
    EMBL; M31160; AAB05637.1; -.
DR
    PIR; A41918; A41918.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FΤ
    NON TER
             1
FT
    SIGNAL
                    1
                            POTENTIAL.
              <1
FT
    PROPEP
              2
                    259
                           POTENTIAL.
                  373
277
FΤ
              260
                           TRANSFORMING GROWTH FACTOR BETA 1.
    CHAIN
    DISULFID 266
FT
                           BY SIMILARITY.
                          BY SIMILARITY.
FT
    DISULFID 276 339
FT
    DISULFID 305 370
                           BY SIMILARITY.
FT
    DISULFID 309 372
                           BY SIMILARITY.
    DISULFID 338
                   338
                           INTERCHAIN (BY SIMILARITY).
FT
FT
    CARBOHYD 54
                   54
                          N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD 109 109
                          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
             153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
224 226 CELL ATTACHMENT SITE (POTENTIAL).
FT
    CARBOHYD
FT
    SITE
SQ
    SEQUENCE 373 AA; 42634 MW; 9903F3479C8552E5 CRC64;
 Query Match
                     50.1%; Score 1059.5; DB 1; Length 373;
 Best Local Similarity 54.5%; Pred. No. 1.5e-76;
 Matches 208; Conservative 52; Mismatches 99; Indels 23; Gaps
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
QУ
           2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
         90 GES-VEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
             62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWOPOSHSIFFVFNVSRARRG-GRPT 120
Db
        149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
            Db
        121 LLHRAELRMLRQKAAADSAGTEORLELYOGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
        204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEO-ORGDMOSIAKKHRRVPYV 239
Db
        259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316
Qу
            Db
        240 LAMALPAERANELHSARRRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLQW 291
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Qу
         317 KWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALEPLPIVY 376
             Db
         292 KWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDPLPIIY 351
QУ
         377 YVGRKPKVEQLSNMIVRSCKCS 398
             Db
         352 YVGRNVRVEQLSNMVVRACKCS 373
RESULT 12
TGF1 XENLA
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                  STANDARD;
                              PRT; 382 AA.
AC
    P16176:
    01-APR-1990 (Rel. 14, Created)
DT
    01-APR-1990 (Rel. 14, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).
DE
OS
    Xenopus laevis (African clawed frog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC
    Xenopodinae; Xenopus.
OX
    NCBI TaxID=8355;
RN
    [1]
RΡ
    SEOUENCE FROM N.A.
RX
    MEDLINE=90110090; PubMed=2295601;
RA
    Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B.,
RA
    Sporn M.B., Melton D.A.;
RT
    "Identification of a novel transforming growth factor-beta (TGF-beta
RT
    5) mRNA in Xenopus laevis.";
RL
    J. Biol. Chem. 265:1089-1093(1990).
RN
    [2]
RP
    SEQUENCE FROM N.A.
RA
    Vempati U.D., Kondaiah P.;
RL
    Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
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    use by non-profit institutions as long as its content is in no way
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    modified and this statement is not removed. Usage by and for commercial
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CC
    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; J05180; AAA49968.1; -.
    EMBL; AF009335; AAB64441.1; -.
DR
DR
    EMBL; AF009331; AAB64441.1; JOINED.
DR
    EMBL; AF009332; AAB64441.1; JOINED.
    EMBL; AF009333; AAB64441.1; JOINED.
DR
DR
    EMBL; AF009334; AAB64441.1; JOINED.
DR
    PIR; A34929; B61036.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
```

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DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      21
                              POTENTIAL.
FT
    PROPEP
                22
                     270
FT
    CHAIN
               271
                     382
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
               277
                     286
                              BY SIMILARITY.
FT
    DISULFID
               285
                     348
                              BY SIMILARITY.
FΤ
    DISULFID
               314
                     379
                              BY SIMILARITY.
FT
    DISULFID
               318
                     381
                              BY SIMILARITY.
FT
    DISULFID
               347
                     347
                              INTERCHAIN (BY SIMILARITY).
FΤ
    CARBOHYD
               73
                     73
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
               123
                     123
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
               166
                     166
FT
                              CELL ATTACHMENT SITE (POTENTIAL).
    SITE
               234
                     236
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              382 AA; 44200 MW; 1034621C917AAE15 CRC64;
 Query Match
                       41.3%; Score 873; DB 1; Length 382;
 Best Local Similarity 46.9%; Pred. No. 9.2e-62;
 Matches 190; Conservative 55; Mismatches 122; Indels 38; Gaps
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Qу
           9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
            : : | | | | | | | |
                          Db
          1 MEVLWMLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
          69 PPGPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDK 123
Qу
                   : ||||| : : :: |
                                          : ||||:|| || ::|
          60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
Db
         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEOHVELYOKYSNDSW-- 179
Qу
                      116 ----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKOTDKNMDORMELFWKYOENGTTH 170
Dh
         180 -RYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
Qу
                         171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
Db
         236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYC 293
Qу
                   : | : | : : : | | | | : | | : | : |
Dh
         227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR-----GVGQEYC 277
         294 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 353
Qу
                 Db
         278 FGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVLSLYNQ 337
         354 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            338 NNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382
Db
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RESULT 13
TGF3 CHICK
ΙD
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                   STANDARD;
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                                       412 AA.
AC
    P16047:
DT
    01-APR-1990 (Rel. 14, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
OS
    Gallus gallus (Chicken).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
    Gallus.
OX
    NCBI TaxID=9031;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=89096966; PubMed=3211158;
RA
    Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
    "Complementary deoxyribonucleic acid cloning of a novel transforming
RT
RT
    growth factor-beta messenger ribonucleic acid from chick embryo
RT
    chondrocytes.";
    Mol. Endocrinol. 2:747-755(1988).
RL
RN
    [2]
RΡ
    SEQUENCE FROM N.A.
RC
    STRAIN=White leghorn:
RX
    MEDLINE=95169270; PubMed=7865129;
RA
    Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
RT
    "The chicken transforming growth factor-beta 3 gene: genomic
RT
    structure, transcriptional analysis, and chromosomal location.";
RL
    DNA Cell Biol. 14:111-123(1995).
RN
RP
    SEQUENCE OF 1-117 FROM N.A.
RC
    STRAIN=White leghorn; TISSUE=Blood;
RX
    MEDLINE=92134496; PubMed=1840616;
RA
    Burt D.W., Dey B.R., Paton I.R.;
RT
    "Comparative analysis of human and chicken transforming growth
RT
    factor-beta 2 and -beta 3 promoters.";
RL
    J. Mol. Endocrinol. 7:175-183(1991).
RN
    [4]
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RΡ
RX
    MEDLINE=93024487; PubMed=1406706;
RA
    Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J.,
    Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
RA
RT
    "Identification and characterization of the chicken transforming
    growth factor-beta 3 promoter.";
RT
RL
    Mol. Endocrinol. 6:1285-1298(1992).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
     CC
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    the European Bioinformatics Institute. There are no restrictions on its
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; M31154; AAA49089.1; -.
DR
    EMBL; X58127; CAA41128.2; -.
    EMBL; X60055; CAA41128.2; JOINED.
DR
    EMBL; X60091; CAA41128.2; JOINED.
DR
    EMBL; X60090; CAA41128.2; JOINED.
DR
DR
    EMBL; S46000; AAB23575.1; -.
    PIR; A34939; A34939.
DR
    HSSP; P10600; 1TGJ.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
               1
                    23
                           POTENTIAL.
    PROPEP
              24
                    300
FT
FT
    CHAIN
              301
                   412
                            TRANSFORMING GROWTH FACTOR BETA 3.
FT
    DISULFID
             307 316
                           BY SIMILARITY.
FT
    DISULFID
             315 378
                           BY SIMILARITY.
    DISULFID
             344 409
                           BY SIMILARITY.
FT
            348
                  411
                           BY SIMILARITY.
FT
    DISULFID
            377 377
74 74
135 135
FT
                            INTERCHAIN (BY SIMILARITY).
    DISULFID
FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
FT
    CARBOHYD
             142 142
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
             261 263
                           CELL ATTACHMENT SITE (POTENTIAL).
                           ELPT -> DFRQ (IN REF. 1).
FT
    CONFLICT
             323 326
    SEQUENCE 412 AA; 47077 MW; 1CAB883170069D55 CRC64;
SQ
 Query Match
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 Best Local Similarity 46.4%; Pred. No. 1.9e-60;
 Matches 195; Conservative 56; Mismatches 117; Indels 52; Gaps
Qу
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
            Db
          9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNOIYDKF 124
Qу
             67 YQILALYNSTRELL--EEMEEEKEESCSQENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
Db
Qу
        125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
            125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
Db
        178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
Qу
              181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240
Db
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Qу
        230 N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAOH--LHSSRHRR 278
            -
               Db
        241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300
        279 DYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIW 338
Qу
                   Db
        301 -----ALDTNYCFRNLEENCCVRPLYIELPTDLGWKWVHEPKGYFANFCSGPCPYLR 352
Qу
        339 SLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Dh
        353 SADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
RESULT 14
TGF3 PIG
ID
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AC
    P15203;
DT
    01-APR-1990 (Rel. 14, Created)
DT
    01-APR-1990 (Rel. 14, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DΕ
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
OS
    Sus scrofa (Pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC
OX
    NCBI TaxID=9823;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Ovary;
RX
    MEDLINE=89091120; PubMed=3208746;
RA
    Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,
RA
    Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA
    Chen E.Y.;
RT
    "A new type of transforming growth factor-beta, TGF-beta 3.";
RL
    EMBO J. 7:3737-3743(1988).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    CC
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    or send an email to license@isb-sib.ch).
CC
CC
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DR
    EMBL; X14150; CAA32363.1; -.
DR
    PIR; S01825; S01825.
DR
    HSSP; P10600; 1TGJ.
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
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DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      18
                              POTENTIAL.
FT
    PROPEP
               19
                     297
FT
    CHAIN
               298
                     409
                              TRANSFORMING GROWTH FACTOR BETA 3.
FT
    DISULFID
               304
                     313
                              BY SIMILARITY.
FT
    DISULFID
                     375
                              BY SIMILARITY.
               312
FT
    DISULFID
               341
                     406
                              BY SIMILARITY.
FΤ
    DISULFID
               345
                     408
                              BY SIMILARITY.
                              INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
               374
                     374
FT
    CARBOHYD
               72
                     72
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               133
                     133
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               140
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                     140
                              CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
               259
                     261
              409 AA; 46814 MW; B4900235B5CC955E CRC64;
SO
    SEQUENCE
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 Matches 190; Conservative 58; Mismatches 122; Indels
                                                         47: Gaps
                                                                    14:
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
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Db
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNOIYDKFKG 126
Qу
                       65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
Db
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                                | | | | | : | | :
                                               : || :||:|
                :: || | : :
         125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Db
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             : | :|
         181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
Db
         231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAOH--LHSSRHRRDYK 281
Qу
               : :: | :|
                           241 QEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAQRKKR--- 297
Db
         282 DDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD 341
Qу
                 Db
         298 ----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSAD 352
         342 TOYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
             Dh
         353 TTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVVKSCKCS 409
RESULT 15
TGF3 MOUSE
ID
    TGF3 MOUSE
                 STANDARD;
                               PRT;
                                    410 AA.
AC
    P17125;
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01-AUG-1990 (Rel. 15, Created)
DT
DT
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 3 precursor (TGF-beta 3).
DΕ
GN
    TGFB3.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RX
    MEDLINE=90190650; PubMed=2628730;
RA
    Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT
    "Complementary DNA cloning of the murine transforming growth
RT
    factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT
    of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT
    adult tissues.";
    Mol. Endocrinol. 3:1926-1934(1989).
RL
RN
    [2]
RΡ
    SEQUENCE FROM N.A.
    MEDLINE=91000714; PubMed=2206556;
RX
    Denhez F., Lafyatis R., Kondaiah P., Roberts A.B., Sporn M.B.;
RA
    "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT
RT
    mTGF-beta 3.";
RL
    Growth Factors 3:139-146(1990).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    ______
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
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    modified and this statement is not removed. Usage by and for commercial
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    or send an email to license@isb-sib.ch).
CC
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DR
    EMBL; M32745; AAA40422.1; -.
DR
    PIR; A41397; A41397.
DR
    HSSP: P10600; 1TGJ.
DR
    MGD; MGI:98727; Tqfb3.
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb_N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
                1 23 POTENTIAL.
    SIGNAL
    PROPEP
                       298
FT
                24
                                POTENTIAL.
FT
    CHAIN
                299 410
                               TRANSFORMING GROWTH FACTOR BETA 3.
```

```
FT
    DISULFID
              305
                    314
                            BY SIMILARITY.
FT
    DISULFID
              313
                    376
                            BY SIMILARITY.
FT
    DISULFID
                    407
              342
                            BY SIMILARITY.
FT
    DISULFID
                    409
              346
                            BY SIMILARITY.
FT
    DISULFID
              375
                    375
                            INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
              72
                    72
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              133
                    133
FT
    CARBOHYD
              140
                    140
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
              259
                    261
                            CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE
             410 AA; 46884 MW; 250F7048CA432BD6 CRC64;
 Query Match
                     39.5%; Score 835; DB 1; Length 410;
 Best Local Similarity 45.2%; Pred. No. 1e-58;
 Matches 188; Conservative 58; Mismatches 126; Indels 44; Gaps
                                                                13;
Qу
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
            Db
          7 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP 64
Qу
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNOIYDKFKG 126
             Db
         65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEOHVELYOKYSND----S 178
Qу
               :: || | : :
                           | ||| |:||:
                                          : || :||:|
        125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
Db
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
            Db
        181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFOPNGDILENV 240
        231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
Qу
              : :: | ::
                           Db
        241 HEVMEIKFKGVDNEDDHGRGDLGRLKKOKDHHNPHLILMMIPPHRLDSPGOGSORK---- 296
        283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
Qу
              Db
        297 -- KRALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADT 354
        343 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        355 THSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 410
```

Search completed: October 28, 2003, 09:08:38 Job time: 9.97725 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 07:50:55; Search time 31.909 Seconds (without alignments) 3218.683 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:\*

1: sp\_archea:\*

2: sp\_bacteria:\*
3: sp fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

0\_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		<del>ह</del>				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	1820	86.1	390	6	Q9TUM8	Q9tum8 equus cabal
2	1741	82.4	368	11	Q8R4D9	Q8r4d9 sigmodon hi
3	848	40.1	379	13	Q8JHF5	Q8jhf5 sparus aura
4	844	39.9	379	13	Q8AXK8	Q8axk8 sparus aura
5	835	39.5	412	11	Q91YU7	Q91yu7 mus musculu
6	828.5	39.2	414	11	Q91VP5	Q91vp5 mus musculu
7	824.5	39.0	382	13	Q9PWA9	Q9pwa9 morone chry
8	808.5	38.2	382	13	093449	093449 oncorhynchu
9	782.5	37.0	376	13	Q9PTQ2	Q9ptq2 cyprinus ca
10	767.5	36.3	399	11	Q9ERB7	Q9erb7 mesocricetu
11	727	34.4	362	11	Q99K17	Q99k17 mus musculu

```
130 11 Q08714
12
      696
           32.9
                                                  008714 mesocricetu
13
      681
           32.2
                   361 13 098854
                                                  Q98854 cyprinus ca
14
      679
           32.1
                  124 6 O95N80
                                                 Q95n80 canis famil
15
      638
           30.2
                  112 6 002730
                                                 002730 oryctolagus
16
    607.5
           28.7
                  255 11 0921T1
                                                  Q921t1 mus musculu
           27.9
17
      589
                  127 6 O9TV08
                                                 Q9tv08 canis famil
                  224 11 Q8CDZ9
18
    577.5
           27.3
                                                  Q8cdz9 mus musculu
                  200 13 Q90YF1
19
     557
           26.3
                                                  Q90yf1 pleuronecte
           26.2
20
      554
                  101 11 Q9R184
                                                  Q9r184 meriones un
21
   463.5
          21.9 179 13 Q90YF2
                                                  Q90yf2 pleuronecte
22
     413
          19.5
                  88 13 Q90YF5
                                                  Q90yf5 pleuronecte
23
     402
          19.0
                  88 13 Q90YF7
                                                  Q90yf7 oncorhynchu
                  88 13 Q90ZE7
24
     397
          18.8
                                                  Q90ze7 acipenser b
                  87 13 042306
25
          18.6
     393
                                                  042306 carassius a
           18.1
17.9
                   91 6 O9MYZ1
26
      383
                                                 Q9myzl capra hircu
                  309 4 Q8WV88
27
      379
                                                 Q8wv88 homo sapien
      373
28
           17.6 86 6 Q28241
                                                 Q28241 cervus elap
29
      358
           16.9
                   81 6 Q9N1S3
                                                 Q9n1s3 capreolus c
30
      352
           16.7
                   375 13 Q8UWD8
                                                  Q8uwd8 columba liv
31
      339
          16.0
                  375 13 Q8AVB2
                                                  O8avb2 coturnix co
32
     337
           15.9
                  375 13 Q8UWD7
                                                  Q8uwd7 coturnix ch
                  375 13 Q98SP0
33
     332
           15.7
                                                  Q98sp0 gallus gall
                   375 6 Q9GM97
34
      329
           15.6
                                                 Q9qm97 equus cabal
35
      329
           15.6
                   375 13 Q8UWE0
                                                  Q8uwe0 anas platyr
          15.6
36
      329
                  389 13 Q90YY0
                                                  Q90yy0 ictalurus p
37
     327
          15.5 375 13 Q8UWD9
                                                  Q8uwd9 anser anser
38
     325
          15.4 375 6 Q8HY52
                                                 08hy52 lepus capen
39
     322
          15.2 375 6 Q95J86
                                                Q95j86 macaca fasc
                  87 13 Q8JHB6
40
     320
          15.1
                                                  Q8jhb6 scophthalmu
                   77 13 O90YF8
41
      317
          15.0
                                                  Q90yf8 oncorhynchu
42
      312
           14.8
                   375
                      6 Q8WNS6
                                                 08wns6 bos taurus
43
    307.5
          14.5
                   376 13 Q98TB4
                                                  Q98tb4 oreochromis
44
    306.5
          14.5
                  376 13 Q90W06
                                                  Q90w06 umbrina cir
45
    303.5 14.4
                   385 13 Q90W05
                                                  Q90w05 sparus aura
```

## ALIGNMENTS

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RESULT 1
Q9TUM8
ΙD
     Q9TUM8
                 PRELIMINARY;
                                    PRT:
                                           390 AA.
AC
     Q9TUM8;
DT
     01-MAY-2000 (TrEMBLrel. 13, Created)
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
     Transforming growth factor beta 1.
GN
     TGFB1.
ÓS
     Equus caballus (Horse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX
    NCBI TaxID=9796;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Nixon A.J., Brower-Toland B.T., Sandell L.J.;
RT
     "Molecular cloning of equine transforming growth factor beta 1 reveals
RT
     a divergent nucleotide structure that encodes a novel bioactive
```

```
RT
    peptide among mammalian species.";
RL
    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF175709; AAD49431.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb_N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
SO
    SEQUENCE
             390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;
 Query Match
                      86.1%; Score 1820; DB 6; Length 390;
 Best Local Similarity 87.4%; Pred. No. 6.5e-154;
 Matches 348; Conservative 12; Mismatches
                                         30; Indels
                                                          Gaps
                                                      8;
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
             Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
                  121 YKTVETGSHSIYMFFNASELRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGLRLSAHCPCDSKDNTLRVGINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 SSRRGDLATIDGMNRPFLLLMATPLERAOOLHSSRHRR-----ALDTNYCSSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            ďU
        353 APCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 2
08R4D9
ΙD
    Q8R4D9
              PRELIMINARY;
                             PRT:
                                   368 AA.
AC
    Q8R4D9;
DT
    01-JUN-2002 (TrEMBLrel. 21, Created)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
```

```
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta-1 protein (Fragment).
GN
OS
    Sigmodon hispidus (Hispid cotton rat).
OC.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC
    Sigmodon.
OX
    NCBI_TaxID=42415;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Blanco J.C., Pletneva L.M., Prince G.A.;
RT
    "Cotton rat cytokines, chemokines, and interferons.";
RL
    Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
DR
    EMBL; AF480858; AAL87199.1; -.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
FT
    NON TER
                1
                     1
SO
    SEOUENCE
             368 AA; 41905 MW; A5C91207B0468B4A CRC64;
 Query Match
                      82.4%; Score 1741; DB 11; Length 368;
 Best Local Similarity 86.4%; Pred. No. 6.7e-147;
 Matches 325; Conservative 16; Mismatches
                                          27; Indels
                                                       8; Gaps
                                                                  1;
         23 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYN 82
Qу
            1 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYN 60
Db
         83 STRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELRE 142
Qу
            61 STRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDIPHSVYMFFNTSDIRE 120
Db
        143 AVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTG 202
Qу
            Db
        121 AVPEPPLLSRAELRLQRFKSNVEQHVELYEKYSNNSWRYLGNRLLSPTDSPEWLSFDVTS 180
Qу
        203 VVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMA 262
            Db
        181 VVRKWLNQGDGIQGFRFSAHCSCDSKDNILHVEINGISPKRRGDLGTIHDMNRPFLLLMA 240
        263 TPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEP 322
Qу
                                Db
        241 TPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEP 292
        323 KGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKP 382
Qу
            293 KGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKP 352
Db
        383 KVEQLSNMIVRSCKCS 398
Qу
            111111111
```

```
RESULT 3
O8JHF5
ΙD
    Q8JHF5
                PRELIMINARY:
                                 PRT;
                                        379 AA.
AC
    Q8JHF5;
DT
     01-OCT-2002 (TrEMBLrel. 22, Created)
DT
     01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT
     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta 1.
OS
     Sparus aurata (Gilthead sea bream).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
    Sparidae; Sparus.
OX
    NCBI_TaxID=8175;
RN
     [1]
RP
    SEQUENCE FROM N.A.
RA
    Tafalla C., Aranguren R., Secombes C.J., Castrillo J.L., Novoa B.,
     Figueras A.;
RA
RT
     "Molecular characterization of sea bream (Sparus aurata) transforming
RT
    growth factor betal.";
RL
    Fish and Shellfish Immunol. 0:0-0(2002).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF510084; AAN03842.1; -.
DR
     InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
     InterPro; IPR001111; TGFb N.
DR
     InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 2.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
     ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA_1; 1.
DR
SQ
    SEQUENCE 379 AA; 43506 MW; COC9D3D2FCA29C0E CRC64;
 Query Match
                         40.1%; Score 848; DB 13; Length 379;
 Best Local Similarity
                         46.5%; Pred. No. 3.5e-67;
 Matches 186; Conservative 68; Mismatches 110; Indels
                                                              36; Gaps
Qу
          12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
                                                             | | | | |
             ]: |:::: | |: ::|:|||||:|:|:||:||:|||
Db
           3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPTESPQAGD--E 59
          71 GPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDKFK 125
Qу
               : | :|:|
                                                      111
Db
          60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEQEEEEYFA---TRVHKFNTTNPV----- 111
Qу
         126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYQKYSNDSWRYL 182
              \\ :: \ \\ \\\:\ :: : \\\:\\\:\\:\\
                                                     112 RTPQNMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEQRVELYQGLGT-SPRYL 169
Db
Qу
         183 SNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
             :: :
```

```
Db
        170 ASRFITNELRDKWLSFDVTETLQNWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
Qу
        241 SGRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTE 298
            230 AG-RGDKAVLDDMTKOPPYILTMSIPKNVSSHL-TSRKKRSTETKDT-----CTAOTE 280
Db
        299 KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGA 358
Qу
              281 -TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSQILALYKHHNPGA 339
Db
        359 SAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        340 SAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 379
RESULT 4
Q8AXK8
ID
    O8AXK8
              PRELIMINARY;
                              PRT;
                                    379 AA.
AC
    Q8AXK8;
DT
    01-MAR-2003 (TrEMBLrel. 23, Created)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DΕ
    Transforming growth factor beta 1.
OS
    Sparus aurata (Gilthead sea bream).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopteryqii; Percomorpha; Perciformes; Percoidei;
OC.
    Sparidae; Sparus.
OX
    NCBI TaxID=8175;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RA
    Tafalla C., Novoa B., Aranguren R., Figueras A.;
    "Molecular cloning and characterization of sea bream (Sparus aurata)
RT
RT
    TGF beta 1.";
RL
    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF424703; AAN76665.1; -.
    SEQUENCE 379 AA; 43485 MW; A306EC387F6DBA7C CRC64;
SQ
 Query Match
                      39.9%; Score 844; DB 13; Length 379;
 Best Local Similarity
                      46.5%; Pred. No. 8.1e-67;
 Matches 186; Conservative 67; Mismatches 111; Indels
                                                       36: Gaps
                                                                  15:
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
Qу
            Db
          3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPTESPQAGD--E 59
         71 GPLPEAVLALYNSTRDRVAGESVEPEPE----PEADYYAKEVTRVLMVESGNQIYDKFK 125
Qу
              : | :
ďu
         60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEXEEEEYFA---TRVHKFNTTNPV----- 111
Qу
        126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYOKYSNDSWRYL 182
             Db
        112 RTPQNMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEQRVELYOGLGT-SPRYL 169
Qу
        183 SNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
                     | :|
Db
        170 ASRFITNELRDKWLSFDVTETLQNWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
```

```
Qу
         241 SGRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTE 298
            Db
         230 AG-RGDKAVLDDMTKQPPYILTMSIPKNVSSHL-TSRKKRSTETKDT-----CTAQTE 280
         299 KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGA 358
Oy
              Db
         281 -TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSOXLALYKHHNPGA 339
         359 SAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
            Db
         340 SAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 379
RESULT 5
Q91YU7
ID
    Q91YU7
               PRELIMINARY;
                           PRT:
                                     412 AA.
AC
    Q91YU7;
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
DT
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DΕ
    Transforming growth factor, beta 3.
GN
    TGFB3.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RР
    SEQUENCE FROM N.A.
RA
    Strausberg R.;
RL
    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
DR
    EMBL; BC014690; AAH14690.1; -.
DR
    MGD; MGI:98727; Tgfb3.
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
SO
    SEQUENCE 412 AA; 47144 MW; F3EB65D046DF32AD CRC64;
 Query Match
                       39.5%; Score 835; DB 11; Length 412;
 Best Local Similarity 45.2%; Pred. No. 5.8e-66;
 Matches 188; Conservative 58; Mismatches 126; Indels 44; Gaps
                                                                    13;
Qу
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                     Db
          9 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGOILSKLRLTSPPEPSVMT--HVP 66
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
Qу
```

```
Db
         67 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 126
Qу
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYOKYSND----S 178
                                             : [] : [] :
                Db
         127 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFOILRPDEHIAK 182
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             Db
         183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFOPNGDILENV 242
Qу
         231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
              Db
         243 HEVMEIKFKGVDNEDDHGRGDLGRLKKOKDHHNPHLILMMIPPHRLDSPGOGSORK---- 298
Qу
         283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
               299 -- KRALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADT 356
Db
Qу
         343 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         357 THSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
RESULT 6
091VP5
               PRELIMINARY;
                              PRT; 414 AA.
ID
    091VP5
AC
    Q91VP5;
    01-DEC-2001 (TrEMBLrel. 19, Created)
DΤ
DT
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
    Similar to transforming growth factor, beta 2.
GN
    TGFB2.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RC
    TISSUE=Breast tumor;
RA
    Strausberg R.;
    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RL
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; BC011170; AAH11170.1; -.
    MGD; MGI:98726; Tqfb2.
DR
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
DR
    Ptam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
SQ
    SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;
```

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Query Match 39.2%; Score 828.5; DB 11; Length 414; Best Local Similarity 44.2%; Pred. No. 2.2e-65;
 Matches 188; Conservative 63; Mismatches 121; Indels 53; Gaps
                                                                  15:
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGDVP-P 70
Qу
                5 VLSTFLLLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEP 60
Db
         71 GPLPEAVLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNOIYD 122
Qу
              Db
         61 DEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHLPSENAIPP 120
        123 KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----K 173
QУ
             121 TFY-RPYFRIVRFDVSTMEKNASN---LVKAEFRVFRLQNPKARVAEQRIELYQILKSKD 176
Dh
        174 YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSS----- 225
Qу
             :: : ||: ::::
                             177 LTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLHHKDRNLGFKISLHCPCCTFVPSNN 236
Db
        226 ---DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHS 273
Qу
                         Db
        237 YIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLESQOS 296
        274 SRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 333
QУ
                      Db
        297 SRRKK-----RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGA 349
        334 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 393
Qу
            Db
        350 CPYLWSSDTOHTKVLSLYNTINPEASASPCCVSQDLEPLTILYYIGNTPKIEQLSNMIVK 409
Qу
        394 SCKCS 398
            Db
        410 SCKCS 414
RESULT 7
O9PWA9
ID
    Q9PWA9
              PRELIMINARY;
                              PRT;
                                    382 AA.
AC
    Q9PWA9;
DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
GN
    TGF-BETA.
OS
    Morone chrysops x Morone saxatilis (white bass x striped bass).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ÚĊ
    Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
    Moronidae; Morone.
    NCBI TaxID=45352;
OX
RN
    [1]
RΡ
    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
    TISSUE=KIDNEY;
RX
    MEDLINE=20394636; PubMed=10938723;
RA
    Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
```

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Tompkins W.A.F.;
RT
     "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT
    chrysops) transforming growth factor-beta (TGF-beta), and development
RT
    of a reverse transcription quantitative competitive polymerase chain
RT
    reaction (RT-qcPCR) assay to measure TGF-beta mRNA of teleost fish.";
RL
    Fish Shellfish Immunol. 10:61-85(2000).
     -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
    -!- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC
CC
        PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF140363; AAD46997.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                 1
                        ?
                               POTENTIAL.
FT
                 ?
    PROPEP
                      270
FT
    CHAIN
                271
                      382
                               TRANSFORMING GROWTH FACTOR BETA.
FT
    DISULFID
               278
                      286
                               BY SIMILARITY.
                               BY SIMILARITY.
FT
    DISULFID
                285
                      348
FT
    DISULFID
               314
                      379
                               BY SIMILARITY.
             318
FT
    DISULFID
                     381
                              BY SIMILARITY.
FT
    DISULFID
             347 347
                               INTERCHAIN (BY SIMILARITY).
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                73
                      73
FT
    CARBOHYD
              108
                     108
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
    CARBOHYD
               113
                      113
FT
    CARBOHYD
               124
                      124
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               259
                      259
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
               235
                      237
                               CELL ATTACHMENT SITE (POTENTIAL).
    SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;
SQ
 Query Match
                        39.0%; Score 824.5; DB 13; Length 382;
 Best Local Similarity 46.1%; Pred. No. 4.5e-65;
 Matches 184; Conservative 64; Mismatches 114; Indels
                                                            37: Gaps
                                                                       14;
Qу
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL---ASPPSQGDVPPG 71
             ďŪ
           6 LMLVVVYTVGN-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPKEPEPDQAGDEEEI 64
          72 PLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDKFKG 126
Qу
             Db
          65 PTP--LLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAKVLHKFNMTRKNN----- 114
Qу
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV--EQHVELYQKYSNDSWRYLSN 184
              Db
         115 TDTTKKMFFNISEIRESVGDYRLLTSAELRMLIKKTTIYDEQRVELYSGL-GDSPRYLAS 173
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RA

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185 RLLAPSDSPEWLSFDVTGVVROWLTRREAIEGF--RLSAHSSSDSKDNTL-HVEINGFNS 241
Qу
                      :||||| :: || : :|| ||
                                                  : | |:
         174 RFITNKWKDKWLSFDVTKTLQDWLKGTDDEQGFQLRLFCECNKVSAGETIFKFGISGIDP 233
Db
         242 GRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
                    : | : | |
Db
         234 G-RGDTGPMQLLTQQPPYILTMSIP----QNISSPSTSRKKRSTETK----DVCTAQTE- 283
Qу
         300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
              Db
         284 TCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIWNAENKYSQILALYKHHNPGAS 343
Qу
         360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         344 AQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 382
RESULT 8
093449
ID
    093449
                PRELIMINARY;
                                PRT; 382 AA.
AC
    093449; Q91217;
    01-NOV-1998 (TrEMBLrel. 08, Created)
DT
DT
    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
GN
    TGF-BETA OR TGF.
OS
    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC
    Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX
    NCBI TaxID=8022;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=LEUKOCYTE;
RX
    MEDLINE=99242020; PubMed=10227481;
RA
    Daniels G.D., Secombes C.J.;
RT
    "Genomic organisation of rainbow trout, Oncorhynchus mykiss TGF-
RT
    BETA.";
RL
    Dev. Comp. Immunol. 23:139-147(1999).
RN
RΡ
    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
    TISSUE=LEUKOCYTE;
    MEDLINE=98390168; PubMed=9722928;
RX
RA
    Hardie L.J., Laing K.J., Daniels G.D., Grabowski P.S., Cunningham C.,
    Secombes C.J.;
RA
RT
    "Isolation of the first piscine transforming growth factor beta gene:
RT
    analysis reveals tissue specific expression and a potential regulatory
    sequence in rainbow trout (Oncorhynchus mykiss).";
RT
RL
    Cytokine 10:555-563(1998).
CC
    -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY
CC
        MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
    EMBL; AJ007836; CAA07707.1; -.
```

```
DR
    EMBL; X99303; CAA67685.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                     20
                             POTENTIAL.
               1
FT
    PROPEP
                    270
               21
FT
    CHAIN
              271
                    382
                             TRANSFORMING GROWTH FACTOR BETA.
FT
    DISULFID
              278
                    286
                             BY SIMILARITY.
FT
    DISULFID
              285
                    348
                            BY SIMILARITY.
FT
    DISULFID 314
                   379
                            BY SIMILARITY.
FT
    DISULFID 318
                   381
                             BY SIMILARITY.
FT
    DISULFID 347 347
                             INTERCHAIN (BY SIMILARITY).
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
                    76
FT
              76
                  116
    CARBOHYD 116 116
CARBOHYD 125 125
FT
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
FT
    CONFLICT 237 237
                            N \rightarrow D (IN REF. 2).
FT
    CONFLICT 345 345
                             Q \rightarrow H (IN REF. 2).
FT
    CONFLICT
             371
                   372
                             LS -> VP (IN REF. 2).
FT
    CONFLICT 377 377
                            K -> M (IN REF. 2).
             382 AA; 44136 MW; 93BD4D3540084B92 CRC64;
SO
    SEQUENCE
 Query Match
                      38.2%; Score 808.5; DB 13; Length 382;
 Best Local Similarity 47.1%; Pred. No. 1.2e-63;
 Matches 181; Conservative 57; Mismatches 107; Indels
                                                       39; Gaps
                                                                  13;
Qу
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPP---SQGDVPPGPLPEAVLALYNSTRD 86
            Db
         23 MSTCKSLDLELVKRKRIEAIRGQILSKLRLPKEPEIDQEGDTE--EVPASLMSIYNSTVE 80
         87 RVAGESVE-----PEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSEL 140
Qу
             Db
         81 -LSEEQVHTYIPSTQDAEEEA-YFAKEVHKFNMKQSENT-----SKHQI--LFNMSEM 129
        141 REAVPEPVLLSRAELRLL----RLKLKVEOHVELYOKYSNDSWRYLSNRLLAPSDSPEWL 196
Qу
            Db
        130 RSVLGTDRLLSQAELRLLIKNHGLLDDSEQRLELYRGV-GDKARYLKSHFVSKEWANRWV 188
        197 SFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATI -- HGMN 254
Qу
            []]];
                           : [ ] : [
                                             :|:| | |: |:
Db
        189 SFDVTQTLNEWLQGAGEEQGFQLKLPCDCGKPMEEFRFKISGMNK-LRGNTETLAMKMPS 247
Qу
        255 RPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDL 314
            Db
        248 KPHILLMSLPVERHSQL-SSRKKRQ-----TTTEEICSDKSESCCVRKLYIDFRKDL 298
Qу
        315 GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPI 374
```

```
Db
         299 GWKWIHEPTGYFANYCIGPCTYIWNTENKYSQVLALYKHHNPGASAQPCCVPQVLEPLPI 358
Qу
         375 VYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         359 IYYVGROHKVEQLSNMIVKSCRCS 382
RESULT 9
Q9PTQ2
ΙD
    Q9PTQ2
                PRELIMINARY;
                                  PRT:
                                         376 AA.
AC
    Q9PTQ2;
DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
OS
    Cyprinus carpio (Common carp).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
    Cyprinidae; Cyprinus.
OX
    NCBI TaxID=7962;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Yin Z., Kuang J.;
RT
    "Molecular cloning of carp transforming growth factor beta 1.";
RL
    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
    -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF136947; AAF22573.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
                        22
                                 POTENTIAL.
                  1
FT
    PROPEP
                 23
                       264
FT
                       376
                                 TRANSFORMING GROWTH FACTOR BETA.
    CHAIN
                265
                                 BY SIMILARITY.
FT
    DISULFID
                272
                       280
FT
                       373
                                 BY SIMILARITY.
    DISULFID
                308
FT
    DISULFID
              312
                       375
                                BY SIMILARITY.
FT
                                 INTERCHAIN (BY SIMILARITY).
    DISULFID
              341
                      341
FT
    CARBOHYD
                76
                       76
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               125
                      125
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
               167
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                      167
FT
    SITE
                230
                       232
                                CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE
               376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;
 Query Match
                         37.0%; Score 782.5; DB 13; Length 376;
 Best Local Similarity 44.5%; Pred. No. 2.5e-61;
 Matches 179; Conservative 67; Mismatches 119; Indels 37; Gaps
                                                                           16;
```

```
Qу
           6 LRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSO 65
            1 MRVESLLLALQCLLGFV--HYSGALSTCSPLDLELIKRKRIEAIRGQILSKLRLSKEPEV 58
Db
         66 GDVPPGP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVESGN 118
Qу
                   :| ::::||| : | :|| :|| :|| :||
          59 DEEKESQNIPAELISVYNSTVELNEEQAAPPEQPKEDPVEEEYYAKEVHKFTIKLMEKNP 118
Db
         119 OIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLK--VEQHVELYQKYSN 176
Qу
                        11:111
Db
         119 ---DKF-----LWFNITDISQTLGLNRIISQVELRLLITTFPDGSEORLELYOVIGN 167
         177 DSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEI 236
Qу
             Db
         168 KS-RYLESRFI--PNQRKWLSFDVTQTLKDWLQRSEAEQGFQLKMADNCDPQ-KTFQLKI 223
Qу
         237 NGFNSGRRGDLATIH-GMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFS 295
                  Db
         224 PGLVL-VRGDTETLAVNMPRPHILVMSLPLDGN---NSSKSRRKROTETDOV-----CTD 274
         296 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 355
Qу
             Db
         275 KSD-GCCVRSLYIDFRKDLGWKWIHEPSGYYANYCTGSCSFVWTSENKYSQVLALYKHHN 333
Qу
        356 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC 397
            Db
        334 PGASAQPCRVPQVLNPLPIFYYVGRQHKVEQLSNMIVKTCKC 375
RESULT 10
O9ERB7
ID
    Q9ERB7
               PRELIMINARY;
                             PRT;
                                    399 AA.
AC
    O9ERB7;
DT
    01-MAR-2001 (TrEMBLrel. 16, Created)
DT
    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
    01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DT
DE
    Transforming growth factor-beta 2 (Fragment).
OS
    Mesocricetus auratus (Golden hamster).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC
    Mesocricetus.
OX
    NCBI TaxID=10036;
RN
RP
    SEQUENCE FROM N.A.
    Ramesh G., Kondaiah P., Seshagiri P.B.;
RA
RT
    "Differential expression and selective localization of transforming
ŘТ
    growth factor-beta isoforms in the hamster uterus during estrous
RT
    cycle.";
RL
    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AY007214; AAG02247.1; -.
DR
    HSSP; P08112; 2TGI.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
```

```
Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
FT
    NON_TER 1 1
             399 399
FT
    NON TER
    SEQUENCE 399 AA; 46078 MW; A6FF8E65EAFD5148 CRC64;
SQ
 Query Match
                    36.3%; Score 767.5; DB 11; Length 399;
 Best Local Similarity 43.1%; Pred. No. 5.9e-60;
 Matches 177; Conservative 60; Mismatches 121; Indels 53; Gaps 15;
         18 LLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEA 76
Qу
           Db
          4 LLHLVP--VALSLSTCSTLDMDOFMRKRIEAIRGOILSKLKLTSPPE--DYPEPDEVPPE 59
         77 VLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTP 128
Qу
           Db
         60 VISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHFPSENAIPPTFY-RP 118
        129 HSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EOHVELYO-----KYSNDSW 179
Qу
           Db
        119 YFRIVRFDVSMMEKNASN---LVKAEFRVFRLONPKARVAEORIELYOILKSKDLTSPTO 175
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSK 228
Qу
                      : :
        176 RYIDSKVVKTRAEGEWLSFDVTDAVHEWLHHKDRNLGFKISLHCPCCTFVPFNNNIIPNK 235
Db
        229 DNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAOHLHSSRHRRD 279
Qу
                  Db
        236 SEELEARFAGIDGTSQHSSGHQETIKSTRKKNSGKTPHLLLMLLPSYRLESQOSNRRKK- 294
        280 YKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWS 339
QУ
                Db
        295 -----RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWS 348
Qу
        340 LDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEOLSNM 390
            Db
        349 SDTOHTKVLSLYNTINPEASASPCCVSHDLEPLTILYYIGNTPKIEOLSNM 399
RESULT 11
Q99K17
ID
    Q99K17
            PRELIMINARY; PRT; 362 AA.
AC
    O99K17;
    01-JUN-2001 (TrEMBLrel. 17, Created)
DT
    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Similar to transforming growth factor, beta 3 (Fragment).
GN
    TGFB3.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
```

```
RA
    Strausberg R.;
RL
    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; BC005513; AAH05513.1; -.
DR
    HSSP: P10600: 1TGJ.
DR
    MGD; MGI:98727; Tgfb3.
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
FT
    NON TER
               1
SQ
    SEQUENCE
             362 AA; 41486 MW; 0808E46180FDAE70 CRC64;
                     34.4%; Score 727; DB 11; Length 362;
 Query Match
 Best Local Similarity 44.0%; Pred. No. 2.1e-56;
 Matches 164; Conservative 52; Mismatches 113; Indels 44; Gaps
         58 RLASPPSQGDVPPGPLPEAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVL 112
Qу
           2 RVGSPPEPSVMT--HVPYQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFD 59
Db
        113 MVE---SGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVE 165
Qу
            Db
         60 MIQGLAEHNELAVCPKGITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTE 115
        166 QHVELYQKYSND----SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSA 221
Qу
            116 QRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISI 175
Db
        222 H-----SSSDSKDN---TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPL 265
Qу
                   176 HCPCHTFOPNGDILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKOKDHHNPHLILMMIPP 235
Db
        266 ERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGY 325
Qу
                            |:
        236 HRLDSPGQGSQRK-----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGY 289
Db
        326 HANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVE 385
Qу
            Db
        290 YANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVE 349
        386 QLSNMIVRSCKCS 398
Qу
            Db
        350 QLSNMVVKSCKCS 362
RESULT 12
008714
              PRELIMINARY; PRT; 130 AA.
ID
    008714
    008714; 070331;
AC
```

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DT
     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN
OS
     Mesocricetus auratus (Golden hamster).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC
    Mesocricetus.
OX
    NCBI TaxID=10036;
RN
RP
     SEQUENCE FROM N.A.
RC
     STRAIN=LVG (SYR);
     MEDLINE=93304479; PubMed=8317544;
RX
RA
     Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA
     Elovic A., McBride J., Gallagher G., Todd R.;
RT
     "Sequential expression of transforming growth factors alpha and beta 1
     by eosinophils during cutaneous wound healing in the hamster.";
RT
     Am. J. Pathol. 143:130-142(1993).
RL
RN
     SEQUENCE OF 26-115 FROM N.A.
RΡ
RC
     STRAIN=SYRIAN; TISSUE=SPLEEN;
RX
     MEDLINE=98234044; PubMed=9573100;
RA
     Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT
     "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
     analysis of cytokine mRNA expression in experimental visceral
RT
RT
     leishmaniasis.";
     Infect. Immun. 66:2135-2142(1998).
RL
CC
     -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
CC
         THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
         REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
         DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC
     -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
CC
DR
     EMBL; X60296; CAA42838.1; -.
DR
     EMBL; AF046214; AAC40099.1; -.
     HSSP; P01137; 1KLA.
DR
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
     ProDom; PD000357; TGFb; 1.
DR
DR
     SMART; SM00204; TGFB; 1.
DR
     PROSITE; PS00250; TGF BETA 1; 1.
KW
     Growth factor; Mitogen; Glycoprotein.
FT
     NON TER
                  1
                         1
     PROPEP
FT
                  <1
                         18
                        130
                                  TRANSFORMING GROWTH FACTOR BETA 1.
FT
     CHAIN
                  19
                        34
FT
     DISULFID
                  25
                                  BY SIMILARITY.
FT
     DISULFID
                  33
                        96
                                  BY SIMILARITY.
FT
    DISULFID
                  66
                       129
                                  BY SIMILARITY.
                        95
FT
    DISULFID
                  95
                                  INTERCHAIN (BY SIMILARITY).
                        93
FT
    CONFLICT
                  93
                                  G \rightarrow S (IN REF. 2).
     SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;
SO
                          32.9%; Score 696; DB 11; Length 130;
  Query Match
  Best Local Similarity 92.0%; Pred. No. 2.8e-54;
```

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Matches 127; Conservative 0; Mismatches 3; Indels 8; Gaps
Qу
         261 MATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIH 320
             Db
           1 MATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIH 52
Qу
         321 EPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGR 380
             Db
          53 EPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASAGPCCVPOALEPLPIVYYVGR 112
         381 KPKVEQLSNMIVRSCKCS 398
Qу
             113 KPKVEQLSNMIVRSYKCS 130
Db
RESULT 13
098854
ΙD
    Q98854
                PRELIMINARY;
                                 PRT;
                                       361 AA.
AC
    Q98854;
DT
    01-FEB-1997 (TrEMBLrel. 02, Created)
DT
    01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DΕ
    Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
GN
    TGFB2.
OS
    Cyprinus carpio (Common carp).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
    Cyprinidae; Cyprinus.
    NCBI TaxID=7962;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=HEART;
RX
    MEDLINE=97354301; PubMed=9210595;
    Sumathy K., Desai K.V., Kondaiah P.;
RA
RT
    "Isolation of transforming growth factor-beta2 cDNA from a fish,
RT
    Cyprinus carpio by RT-PCR.";
RL
    Gene 191:103-107(1997).
CC
    -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC
        DEPENDENT T-CELL GROWTH.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; U66874; AAB62983.1; -.
    HSSP; P08112; 2TGI.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
    NON TER
FT
                1
                        1
FT
    PROPEP
                <1
                      257
               258
                                TRANSFORMING GROWTH FACTOR BETA 2.
FT
    CHAIN
                      361
    DISULFID
               264
FT
                      273
                               BY SIMILARITY.
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DISULFID 272
                    335
                            BY SIMILARITY.
FT
    DISULFID 334 334
                             INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
                   30
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
              30
FT
    CARBOHYD
                    98
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
              98
FT
    CARBOHYD
             199
                    199
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    NON TER
             361
                    361
    SEQUENCE 361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;
SQ
 Query Match
                      32.2%; Score 681; DB 13; Length 361;
 Best Local Similarity 41.3%; Pred. No. 2.7e-52;
 Matches 155; Conservative 55; Mismatches 115; Indels 50; Gaps
Qу
         52 QILSKLRLASPPSQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE----ADYY 104
            1
Db
          1 QILCKLKLSCPP---EIYPEPEEVSRDIIAIYNSTRDLLQEKANERAATCERQRTGEEYY 57
        105 AKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL- 160
Qу
            58 AKEVHKIDMQPFYPAENVIPTKHY-NPYFRRLRFDVSSMEKNASN---LVKAELRIFRLO 113
Db
        161 --KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRRE 212
QУ
             114 NPKARVSEQRIELYQILGHKDLTSPTQRYIDSKVVRTRTEGEWLSFDVTEAVSEWLLHRD 173
Db
        213 AIEGFRLSAHSSS------DSKDNTLHVEINGFNSG--RRGDLATI----HGMNR 255
Qу
                           : | | : | | |
              11::1
                                                         174 RNNGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDDSFVHGGDLKMFKKRRHSGQS 233
Db
        256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
            234 PHLLLMLLPSYRLESQHKS-HRQ-----KRALDAAFCFRNVQDNCCLRSLYIDFKKDLG 286
Db
        316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
            287 WKWIHEPKGYNANFCAGACPYLWSADTOHSNILGLYNTINPEASASPCCVSODLEPLTIL 346
Db
        376 YYVGRKPKVEOLSNM 390
Qу
            | | | : | : | | | | | | | | | |
Db
        347 YYIGKTPKIEOLSNM 361
RESULT 14
095N80
ID
    O95N80
             PRELIMINARY; PRT; 124 AA.
    Q95N80;
AC
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
    Transforming growth factor beta 1 (Fragment).
DΕ
OS
    Canis familiaris (Dog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC
    NCBI TaxID=9615;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RΡ
    Fonfara S., Groene A., Baumgaertner W.;
RA
RT
    "Sequence of canine transforming growth factor beta 1 mRNA in DH82-
```

FT

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RT
     cells.";
RL
     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC
     -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
     EMBL; AF349538; AAK54072.1; -.
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     ProDom; PD000357; TGFb; 1.
     SMART; SM00204; TGFB; 1.
DR
     PROSITE; PS00250; TGF_BETA_1; 1.
DR
FT
    NON TER
                1
FT
    NON TER
                124
                      124
SO
    SEQUENCE
               124 AA; 14329 MW; 21D185218E5556DB CRC64;
  Query Match
                        32.1%; Score 679; DB 6; Length 124;
  Best Local Similarity 93.2%; Pred. No. 8.5e-53;
 Matches 123; Conservative 0; Mismatches
                                                             8; Gaps
                                               l; Indels
                                                                         1;
         264 PLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPK 323
Qу
             Db
           1 PLERAQHLHSSRQRR------ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPK 52
Qу
         324 GYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPK 383
             Db
          53 GYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPK 112
         384 VEQLSNMIVRSC 395
Qу
             Db
         113 VEQLSNMIVRSC 124
RESULT 15
002730
ΙD
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                PRELIMINARY;
                                 PRT;
                                        112 AA.
AC
    002730; 097501;
DТ
     01-JUL-1997 (TrEMBLrel. 04, Created)
     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
DE
    Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN
    TGFB1 OR TGF-BETA-1.
OS
    Oryctolagus cuniculus (Rabbit).
OC.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX
    NCBI TaxID=9986;
RN
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RP
    SEQUENCE FROM N.A.
RA
    Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL
    Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN
    SEQUENCE OF 2-99 FROM N.A.
RP
RA
    Inoue K., Kawabe Y., Kodama T.;
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
        THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
        REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
        DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
```

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CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF000133; AAB53806.1; -.
DR
    EMBL; AB020217; BAA36950.1; -.
DR
    HSSP: P01137: 1KLA.
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein.
KW
FT
    NON TER
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FT
    CHAIN
                1
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                    16
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FT
    DISULFID
               48 111
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FT
    DISULFID
               77
                     77
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FT
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               2
                      3
                             LD \rightarrow FS (IN REF. 2).
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FT
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Search completed: October 28, 2003, 09:12:23

Job time : 33.909 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 1415.77 Seconds

(without alignments)

10489.161 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

Sequence: 1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

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2: gb htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

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16: em fun:\*

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27: em sts:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	339	93.4	1326		AX338213	AX338213 Sequence
2	339	93.4	1605	4	SSTGFBR	Y00111 Porcine mRN
3	339	93.4	1750	4	GGTGFB1	X12373 Porcine mRN
4	339	93.4	2221	4	AF461808	AF461808 Sus scrof
5	339	93.4	3206	4	PIGTGFB1A	M23703 Sus scrofa
6	312.8	86.2	489	6	AX455100	AX455100 Sequence
7	312.8	86.2	1369	4	DOGTGFB1A	L34956 Canine tran
8	312.2	86.0	1173	4	OATGFB1	X76916 O.aries mRN
9	311.8	85.9	1561	9	AGMTGFB	M16658 Simian tran
10	310.2	85.5	339	6	AR036686	AR036686 Sequence
11	310.2	85.5	1560	6	108268	108268 Sequence 2
12	309.2	85.2	1560	6	106216	I06216 Sequence 2
13	309	85.1	1117	4	BOVTGFB	M36271 Bovine tran
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15	308.6	85.0	339	6	A18277	A18277 H.sapiens T
16	308.6	85.0	339	6	A23751	A23751 TGF-betal c
17	308.6	85.0	339	6	A48549	A48549 Sequence 1
18	308.6	85.0	339	6	A48563	A48563 Sequence 1
19	308.6	85.0	339	6	I56854	I56854 Sequence 1
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22	308.6	85.0	699	6	105434	I05434 Sequence 4
23	308.6	85.0	862	6	103312	I03312 Sequence 3
24	308.6	85.0	1176	6	AX481432	AX481432 Sequence
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32	308.6		2745	9	HSTGFB1	X02812 Human mRNA
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    45
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RESULT 1
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LOCUS
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                                                               PAT 09-JAN-2002
DEFINITION Sequence 1 from Patent W00181404.
ACCESSION
           AX338213
           AX338213.1 GI:18128750
VERSION
KEYWORDS
            Sus scrofa (pig)
SOURCE
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  AUTHORS
            Strober, W., Nakamura, K., Kitani, A. and Fuss, I.J.
  TITLE
            Inducible plasmid vector encoding tgf-_g(b) and uses thereof
  JOURNAL
            Patent: WO 0181404-A 1 01-NOV-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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Matches 339; Conservative 0; Mismatches

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SSTGFBR
LOCUS
         SSTGFBR
                           1605 bp
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                                         linear
                                                MAM 27-MAR-1995
DEFINITION Porcine mRNA for transforming growth factor-beta (TFG) precursor.
ACCESSION
        Y00111
         Y00111.1 GI:2129
VERSION
KEYWORDS
         transforming growth factor-beta.
SOURCE
         Sus scrofa (pig)
 ORGANISM Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
           (bases 1 to 1605)
 AUTHORS
        Derynck, R. and Rhee, L.
 TITLE
         Sequence of the porcine transforming growth factor-beta precursor
        Nucleic Acids Res. 15 (7), 3187 (1987)
 JOURNAL
 MEDLINE
         87174844
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Qу

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DEFINITION Porcine mRNA for transforming growth factor-beta 1.
ACCESSION
         X12373
VERSION
         X12373.1 GI:63808
KEYWORDS
         transforming growth factor-beta 1.
SOURCE
         Sus scrofa (pig)
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         Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
           (bases 1 to 1750)
 AUTHORS
         Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
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Nucleotide sequence of chicken transforming growth factor-beta 1

TITLE

YYAKEVTRVLMLESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL

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(TGF-beta 1)
 JOURNAL
          Nucleic Acids Res. 16 (17), 8730 (1988)
 MEDLINE
          88335639
  PUBMED
          3166520
REFERENCE
             (bases 1 to 1750)
 AUTHORS
          Jakowlew, S.B.
 TITLE
          Direct Submission
 JOURNAL
          Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
          health, National Cancer Institute, Laboratory of Chemoprevention,
          Building 41, Room B902, Bethesda, Maryland 20892, USA
COMMENT
          The submitters believe that the chicken cDNA library was
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                              27-MAR-1996.
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RESULT 4
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LOCUS
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DEFINITION Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete
ACCESSION
          AF461808
          AF461808.1 GI:18042250
VERSION
KEYWORDS
          Sus scrofa (pig)
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REFERENCE
             (bases 1 to 2221)
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
          Polymorphism in the porcine transforming growth factor beta 1 gene
 TITLE
 JOURNAL
          Unpublished
REFERENCE
             (bases 1 to 2221)
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
          Direct Submission
 TITLE
 JOURNAL
          Submitted (20-DEC-2001) Institute of Animal Breeding Science,
          University of Bonn, Endenicher Allee 15, Bonn 53115, Germany
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3'UTR 1174. .2221 /gene="TGFB1"

BASE COUNT 504 a 616 c 649 g 452 t

ORIGIN

Query Match 93.4%; Score 339; DB 4; Length 2221; Best Local Similarity 100.0%; Pred. No. 1.3e-60; Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qу Db Qу 85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144 Db 895 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 954 Qу 145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204 955 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1014 Db 205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264 QУ 1015 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 1074 Db 265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324 Qу Db 1075 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1134 325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363 QУ 

RESULT 5 PIGTGFB1A

Db

LOCUS PIGTGFB1A 3206 bp mRNA linear MAM 31-MAR-1995 DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.

1135 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1173

ACCESSION M23703

VERSION M23703.1 GI:755044

KEYWORDS transforming growth factor-beta-1.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 3206)

AUTHORS Kondaiah, P., Van Obberghen-Schilling, E., Ludwig, R.L., Dhar, R.,

Sporn, M.B. and Roberts, A.B.

TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.

Evidence for alternate splicing and polyadenylation

JOURNAL J. Biol. Chem. 263 (34), 18313-18317 (1988)

MEDLINE 89054010 PUBMED 2461367

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Original source text: Sus scrofa (strain miniature swine) cDNA to
         mRNA.
FEATURES
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                1. .3206
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                /mol type="mRNA"
                /strain="miniature swine"
                /db xref="taxon:9823"
                /cell type="peripheral blood lymphocyte"
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                1. .3206
                /gene="TGF-beta-1"
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                906. .2078
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                /codon start=1
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                /db xref="GI:755045"
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                KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
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                3206
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BASE COUNT
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                                 596 t
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 Best Local Similarity
 Matches 339; Conservative 0; Mismatches 0; Indels
                                                  0; Gaps
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QУ
           1800 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1859
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
       1860 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1919
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCCGTGCTGCCGCGCGC
Qу
           Db
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       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
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On Apr 1, 1995 this sequence version replaced gi:341017.

COMMENT

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RESULT 6
AX455100
LOCUS
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                              489 bp
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                                            linear
                                                   PAT 06-JUL-2002
DEFINITION Sequence 167 from Patent W00208453.
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ACCESSION
         AX455100.1 GI:21714285
VERSION
KEYWORDS
         Canis familiaris (dog)
SOURCE
 ORGANISM Canis familiaris
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
         Farr, S.B., Pickett, G.G., Neft, R.E. and Dunn, R.T.
 AUTHORS
 TITLE
         Canine toxicity genes
 JOURNAL
         Patent: WO 0208453-A 167 31-JAN-2002;
         Phase-1 Molecular Toxicology (US)
FEATURES
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                 1. .489
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BASE COUNT
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 Query Match
 Best Local Similarity
                     95.0%; Pred. No. 4.3e-55;
 Matches 323; Conservative
                          0; Mismatches
                                       17: Indels
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         84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
           131 CTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCA 190
Db
        144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
Qу
            191 CGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAA 250
Dh
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCC 263
Qу
           251 GGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCC 310
Db
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
           311 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 370
Db
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           371 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 410
Db
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RESULT 7
DOGTGFB1A
LOCUS
            DOGTGFB1A
                                    1369 bp
                                               mRNA
                                                       linear
                                                                MAM 30-OCT-1994
DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
ACCESSION
            L34956
            L34956.1 GI:516071
VERSION
KEYWORDS
            homologue; transforming growth factor-beta 1.
SOURCE
            Canis familiaris (dog)
 ORGANISM Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
               (bases 1 to 1369)
 AUTHORS
            Manning, A.M., Auchampach, J.A., Drong, R.F. and Slightom, J.L.
  TITLE
            Cloning of a canine cDNA homologous to human transforming growth
            factor-beta 1 (TGFbeta1)
  JOURNAL
            Unpublished (1994)
COMMENT
            Original source text: Canis familiaris adult jugular vein
            endothelial cDNA to mRNA.
FEATURES
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    source
                     /organism="Canis familiaris"
                     /mol type="mRNA"
                     /db xref="taxon:9615"
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                     /tissue type="jugular vein endothelial"
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                     1. .57
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                     /function="anti-inflammatory agent"
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                     /db xref="GI:516072"
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                     KLKAEQHVELYQKYSNDSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFR
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BASE COUNT
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 Best Local Similarity 95.0%; Pred. No. 3.9e-55;
 Matches 323; Conservative 0; Mismatches 17; Indels
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            Db
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           Db
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Qу
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       1191 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1230
RESULT 8
OATGFB1
LOCUS
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                            1173 bp
                                     mRNA
                                           linear
                                                   MAM 18-APR-1995
DEFINITION O.aries mRNA for transforming growth factor-beta I.
ACCESSION
         X76916
VERSION
         X76916.1 GI:496648
KEYWORDS
         TGF-beta 1; transforming growth factor-beta 1.
SOURCE
         Ovis aries (sheep)
 ORGANISM Ovis aries
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
         Bovidae; Caprinae; Ovis.
REFERENCE
 AUTHORS
         Woodall, C.J., McLaren, L.J. and Watt, N.J.
 TITLE
         Sequence and chromosomal localisation of the gene encoding ovine
         latent transforming growth factor-beta 1
 JOURNAL
         Gene 150 (2), 371-373 (1994)
 MEDLINE
         95121932
  PUBMED
         7821809
         2 (bases 1 to 1173)
REFERENCE
 AUTHORS
         Woodall, C.
 TITLE
         Direct Submission
 JOURNAL
         Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
         Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
         Edinburgh EH9 IQH, UK
FEATURES
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                1. .1173
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 Best Local Similarity
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 Matches 326; Conservative
                            0; Mismatches
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Qу
             885 TCGTCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCACGAACCCAA 944
Dh
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Qу
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            1005 GTACAGCAAGGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCATCGGCGGCGCCGTG 1064
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Qу
            1125 GGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1173
Db
RESULT 9
AGMTGFB
LOCUS
                                                       PRI 27-APR-1993
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                               1561 bp
                                                linear
                                        mRNA
DEFINITION Simian transforming growth factor-beta (TGF) mRNA, complete cds.
ACCESSION
          M16658
VERSION
          M16658.1 GI:176552
KEYWORDS
          growth factor; transforming growth factor-beta.
SOURCE
          Cercopithecus aethiops (African green monkey)
 ORGANISM
          Cercopithecus aethiops
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Cercopithecinae; Cercopithecus.
REFERENCE
            (bases 1 to 1561)
 AUTHORS
          Sharples, K., Plowman, G.D., Rose, T.M., Twardzik, D.R. and
         Purchio, A.F.
 TITLE
         Cloning and sequence analysis of simian transforming growth
          factor-beta cDNA
 JOURNAL
         DNA 6 (3), 239-244 (1987)
         87246074
 MEDLINE
  PUBMED
          3474130
COMMENT
          Original source text: African green monkey cells (cell line
          BSC-40), cDNA to mRNA, clone pTGF-beta-2.
FEATURES
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                 /db xref="GI:176553"
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                 KLKVEOHVELYOKYSNNSWRYLSNRLLAPSNSPEWLSFDVTGVVROWLSRGGEIEGFR
                 LSAHCSCDSKDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                 RRALDTNYCFSSTEKNCCVRQLYI DFRKDLGWKWI HEPKGYHANFCLGPCPYI WSLDT
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       1276 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCGTGCCG 1335
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Qу
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1336 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1395
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AR036686
LOCUS
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                                        linear PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5800811.
ACCESSION
        AR036686
VERSION
        AR036686.1 GI:5954542
KEYWORDS
SOURCE
        Unknown.
 ORGANISM Unknown.
        Unclassified.
REFERENCE
        1 (bases 1 to 339)
 AUTHORS
        Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
 TITLE
        Artificial skin prepared from coclagen matrix containing
        transforming growth factor-.beta. having a collagen binding site
        Patent: US 5800811-A 29 01-SEP-1998;
 JOURNAL
FEATURES
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Db
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       121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
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Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
       241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
          301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
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Db

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                                          linear PAT 02-DEC-1994
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DEFINITION Sequence 2 from Patent EP 0373994.
ACCESSION
         I08268
         I08268.1 GI:589017
VERSION
KEYWORDS
SOURCE
         Unknown.
        Unknown.
 ORGANISM
         Unclassified.
           (bases 1 to 1560)
REFERENCE
 AUTHORS
         Purchio, A.F., Gentry, L., Twardzik, D. and Brunner, A.M.
 TITLE
         Cloning and expression of simian transforming growth factor-beta 1
 JOURNAL
         Patent: EP 0373994-A1 2 20-JUN-1990;
FEATURES
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 Best Local Similarity
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           Db
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Qу
           Db
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LOCUS
                                          linear PAT 02-DEC-1994
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DEFINITION
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ACCESSION
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VERSION
         I06216.1 GI:590649
KEYWORDS
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SOURCE

Unknown.

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ORGANISM Unknown.
         Unclassified.
REFERENCE
           (bases 1 to 1560)
 AUTHORS
         Purchio, A.F., Gentry, L. and Twardzik, D.
 TITLE
         Cloning and expression of simian transforming growth factor-SS1
 JOURNAL
         Patent: EP 0293785-A2 2 07-DEC-1988;
FEATURES
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BOVTGFB
LOCUS
         BOVTGFB
                           1117 bp
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                                         linear
                                                MAM 27-APR-1993
DEFINITION Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.
ACCESSION
         M36271
VERSION
         M36271.1 GI:163747
KEYWORDS
         transforming growth factor-beta 1.
SOURCE
         Bos taurus (cow)
 ORGANISM
        Bos taurus
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         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
         Bovidae; Bovinae; Bos.
REFERENCE
         1 (bases 1 to 1117)
 AUTHORS
         Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
         and Baker, C.C.
```

Complementary deoxyribonucleic acid cloning of bovine transforming

TITLE

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growth factor-beta 1
 JOURNAL
         Mol. Endocrinol. 1 (10), 693-698 (1987)
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COMMENT
          Original source text: Bovine fibropapilloma, cDNA to mRNA, (library
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LOCUS
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                                                      MAM 06-MAY-1997
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          partial cds.
ACCESSION
          AF000133
          AF000133.1 GI:2072531
VERSION
KEYWORDS
SOURCE
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 ORGANISM
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          Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
            (bases 1 to 339)
          Taylor, T.K., James, E.R., McGonigle, S. and Yoho, E.R.
 AUTHORS
 TITLE
          Rabbit transforming growth factor beta-1 active region
 JOURNAL
          Unpublished
REFERENCE
            (bases 1 to 339)
 AUTHORS
          Taylor, T.K., James, E.R., McGonigle, S. and Yoho, E.R.
 TITLE
          Direct Submission
 JOURNAL
          Submitted (16-APR-1997) Ophthalmology, Med. Univ. S.C., 171 Ashley
          Avenue, Charleston, SC 29464, USA
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DEFINITION H.sapiens TGF-beta 1 gene seq ID No:1.
ACCESSION
         A18277
VERSION
         A18277.1 GI:513237
KEYWORDS
SOURCE
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REFERENCE
          1 (bases 1 to 339)
 AUTHORS
          Cerletti, N., McMaster, G.K., Cox, D., Schmitz, A. and Meyhack, B.
 TITLE
          Process for the production of biologically active protein (e.g.
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          Patent: EP 0433225-A 1 19-JUN-1991;
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BASE COUNT
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         Db
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Search completed: October 27, 2003, 18:34:44

Job time : 1417.77 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 109.057 Seconds

(without alignments)

8985.201 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

Sequence: 1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

용

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1	339	93.4	1326	24	AAD22696	Porcine transformi
2	312.8	86.2	489	24	ABL99528	Target canine gene
3	311.8	85.9	1303	11	AAQ09317	Monkey transformin
4	311.8	85.9	1559	13	AAQ20289	Sequence encoding
5	311.8	85.9	1561	11	AAQ03268	Simian transformin
6	311.8	85.9	1571	11	AAQ03269	Human transforming
7	310.2	85.5	339	18	AAT42771	TGF-betal active f
8	310.2	85.5	339	20	AAV99375	cDNA encoding a tr
9	310.2	85.5	1560	9	AAN81084	Coding sequence of
10	310.2	85.5	1560	11	AAQ03508	Simian Transformin
11	308.6	85.0	339	17	AAT17235	Human TGF-beta 1 c
12	308.6	85.0	339	20	AAX15245	cDNA encoding the
13	308.6	85.0	650	24	ABK84023	Human cDNA differe
14	308.6	85.0	650	24	ABL68818	Kidney cancer rela
15	308.6	85.0	1176	24	ABZ35738	Human TGF beta 1 p
16	308.6	85.0	1176	24	ABX09981	Human TGFbetal DNA
17	308.6	85.0	1176	24	ABV78162	Human TGF beta 1 D
18	308.6	85.0	1176	24	ABL91703	Human polynucleoti
19	308.6	85.0	1176	25	ABV75391	TGFB1 Arg25Pro pol
20	308.6	85.0	1176	25	ABV75392	TGFB1 Arg25Pro pol
21	308.6	85.0	1569	9	AAN81085	Coding sequence of
22	308.6	85.0	1821	12	AAQ13392	Human pro-TGF-beta
23	308.6	85.0	2537	.1	AAN60972	Sequence encoding
24	308.6	85.0	2537	11	AAQ03301	cDNA encoding huma
25	308.6	85.0	2537	11	AAQ02814	Sequence of pre-TG
26	308.6	85.0	2537	15	AAQ56923	Human pre-TGF-beta
27	308.6	85.0	2537	17	AAT15720	Pre-transforming g
28	308.6	85.0	2537	19	AAV52933	Human pre-transfor
29	308.6	85.0	2742	22	AAI58342	Human polynucleoti
30	308.6	85.0	2745	16	AAT05876	cDNA encoding tran
31	308.6	85.0	2745	22	AAH28216	Nucleotide sequenc

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32
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33
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## ALIGNMENTS

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XX
DT
     26-FEB-2002 (first entry)
XX
     Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
DE
XX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
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PR
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XX
PA
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PΙ
     Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
     WPI; 2002-026155/03.
DR
     P-PSDB; AAE13596.
XX
PT
     Composition for treating autoimmune diseases e.g. inflammatory bowel
```

PT disease in humans, comprises vector containing transforming growth factor-beta under the control of inducible promoter - XX
PS Claim 1; Fig 1; 78pp; English.
XX
CC The invention relates to a composition containing a vector comprising a gene encoding a regulatory transcription factor under the control of a promoter encoding a transforming growth factor-beta (TGF-beta). The vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2

promoter encoding a transforming growth factor-beta (TGF-beta). The vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2 or TGF-beta3, its variants or homologues, by transfecting a cell which is part of a host suspected of having an autoimmune disease, especially inflammatory bowel disease (IBD), under conditions such that the polypeptide encoded by the nucleic acid sequence in the vector is expressed. The vector is delivered using a delivery system. The delivery of the vector results in substantial elimination of symptoms of the autoimmune disease and increased production of IL-10 by the host. The composition is useful for treating various diseases with an autoimmune component such as multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis and psoriasis, and also for assaying the expression of a gene in a cell. The vector is further useful for screening of the effect of test compounds on cytokine (e.g. TGF-beta) expression of transfected cells. The present sequence is a cDNA encoding porcine TGF-betal mutant.

93.4%; Score 339; DB 24; Length 1326;

Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;

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Db
QУ
     145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
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     1090 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1149
Qу
     325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
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CC

XX

SO

Query Match

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AC
    ABL99528;
XX
DT
    02-JUL-2002 (first entry)
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DE
    Target canine gene TGFB1.
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KW
    Canine gene array; toxicological response; ss.
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OS
    Canis sp.
XX
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    WO200208453-A2.
XX
PD
    31-JAN-2002.
XX
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PF
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PR
    21-JUL-2000; 2000US-220057P.
XX
    (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
PΑ
XX
PΙ
    Farr SB, Pickett GG, Neft RE,
                                  Dunn RT;
XX
DR
    WPI; 2002-217063/27.
XX
PT
    Identifying toxicologically relevant canine gene to determine
PT
    toxicological responses of agents, by obtaining and comparing gene
PT
    expression profiles of untreated canine cells and canine cells treated
PT
    with an agent
XX
PS
    Disclosure; Page 67; 140pp; English.
XX
CC
    This invention relates to identifying a toxicologically relevant canine
CC
    gene and the generation of an array of toxicologically relevant
CC
    canine genes. The gene array is useful for obtaining a gene expression
    profile, by exposing a population of cells to an agent, obtaining cDNA
CC
CC
    from the population of cells, labeling the cDNA, and contacting the cDNA
CC
    with the gene array. The relevant gene is useful for making and using
CC
    arrays to determine toxicological responses to various agents, and also
CC
    useful for identifying novel gene sequences and novel canine genes.
CC
    The method for analysing toxicological responses using the canine
CC
    gene array is rapid and efficient. The present sequence is related
CC
    to the canine gene array.
XX
SQ
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 Query Match
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 Best Local Similarity
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 Matches 323; Conservative
                              0; Mismatches
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Db
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            Db
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
            Db
        311 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 370
Qу
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
            371 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 410
Db
RESULT 3
AAQ09317
ID
    AAQ09317 standard; cDNA; 1303 BP.
XX
AC
    AAQ09317;
XX
DT
    25-MAR-2003 (updated)
DT
    12-AUG-1990 (first entry)
XX
DE
    Monkey transforming growth factor-beta cDNA.
XX
KW
    Transforming growth factor-beta; simian; psoriasis;
KW
    TGF-beta.
XX
OS
    Monkey.
XX
                 Location/Qualifiers
FΗ
    Key
FT
    sig_peptide
                 22..63
FT
                 /*tag= a
FT
    mat peptide
                 836..1170
FT
                 /*tag=b
FT
                 /product=monkey transforming growth factor-beta
XX
PN
    EP353772-A.
XX
PD
    07-FEB-1990.
XX
PF
    04-AUG-1989:
               89EP-0114458.
XX
PR
    Ũ5-ĀUĞ-1988;
                88US-0229133.
XX
PΑ
    (ONCO ) ONCOGEN LP.
XX
PΤ
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
    WPI; 1990-038499/06.
DR
DR
    P-PSDB; AAR03743.
ХX
```

```
PT
    used to treat psoriasis by contacting cells with compositions
PT
    containing transforming growth factor-beta.
XX
    Disclosure; fig 1; 20pp; English.
PS
XX
CC
    TGF-beta may be used in the treatment of hyperplasia
CC
    associated with acanthosis-categorised skin diseases, and
CC
    in alleviating psoriatic symptoms associated with cytokine-
CC
    induced phenomena. See also AAQ03268 and AAR03750.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;
                    85.9%; Score 311.8; DB 11; Length 1303;
 Query Match
 Best Local Similarity
                    95.0%; Pred. No. 2.3e-64;
 Matches 322; Conservative
                         0; Mismatches 17; Indels
                                                   0; Gaps
                                                            0;
        Qу
           Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           898 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 957
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           958 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1017
Db
Qу
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264
           1018 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 1077
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       1078 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1137
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1138 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1176
RESULT 4
AAQ20289
   AAQ20289 standard; cDNA; 1559 BP.
ΙD
XX
AC
   AAQ20289;
XX
DT
    25-MAR-2003
              (updated)
DT
   16-APR-1992
             (first entry)
XX
DE
   Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW
   Hypertension therapy; hypotensive agent; blood pressure modulator;
KW
    SS.
XX
```

Inhibition of proliferation of epidermal cells -

PT

```
OS
    Monkey.
XX
FΗ
    Key
                  Location/Qualifiers
FΤ
    CDS
                  262.,282
FΤ
                  /*tag=a
FT
    sig peptide
                  283..324
FT
                  /*taq=b
FT
    CDS
                  325..1098
FT
                  /*tag= c
FT
    mat peptide
                  1099..1436
FT
                  /*tag=d
XX
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
               91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA
XX
PΙ
    Oleson FB, Comereski CR;
XX
    WPI; 1992-024199/03.
DR
    P-PSDB; AAR20124.
DR
XX
PT
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PΤ
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-betal/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
 Query Match
                      85.9%; Score 311.8; DB 13; Length 1559;
 Best Local Similarity 95.0%; Pred. No. 2.3e-64;
 Matches 322; Conservative
                            0; Mismatches 17; Indels
                                                        0; Gaps
                                                                  0;
Qу
         Db
       Qу
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
            1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
```

```
Db
       1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
        Qy
            Db
       1275 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCGTGCCG 1334
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
            Db
       1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            Db
       1395 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1433
RESULT 5
AAQ03268
    AAQ03268 standard; DNA; 1561 BP.
TD
XX
AC
    AAQ03268;
XX
DT
    25-MAR-2003 (updated)
DT
    12-AUG-1990 (first entry)
XX
DΕ
    Simian transforming growth factor-beta cDNA.
XX
KW
    Transforming growth factor-beta; psoriasis; TGF-beta; ss.
XX
OS
    Monkey.
XX
FH
    Key
                 Location/Qualifiers
FT
                 283..324
    sig peptide
FT
                 /*tag= a
FT
                 1096..1431
    mat peptide
FT
                 /*tag=b
FT
                 /product=human transforming growth factor-beta
XX
ΡN
    EP353772-A.
XX
PD
    07-FEB-1990.
XX
PF
    04-AUG-1989; 89EP-0114458.
XX
PR
    05-AUG-1988; 88US-0229133.
XX
    (ONCO ) ONCOGEN LP.
PΑ
XX
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
PΙ
XX
DR
    WPI; 1990-038499/06.
    P-PSDB; AAR03743.
DR
XX
PΤ
    Inhibition of proliferation of epidermal cells -
PT
    used to treat psoriasis by contacting cells with compositions
PT
    containing transforming growth factor-beta.
XX
```

```
XX
CC
   TGF-beta may be used in the treatment of hyperplasia
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
   induced phenomena. See also AAQ03269 and AAR03750.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
                   85.9%; Score 311.8; DB 11; Length 1561;
 Query Match
 Best Local Similarity
                   95.0%; Pred. No. 2.3e-64;
 Matches 322; Conservative 0; Mismatches
                                   17; Indels
                                               0; Gaps
                                                        0;
        Qу
          Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          1156 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1215
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
      1216 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1275
       Qу
          Db
      1276 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 1335
Qу
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG 324
          1336 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1395
Db
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
          Db
      1396 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1434
RESULT 6
AAQ03269
ID
   AAQ03269 standard; DNA; 1571 BP.
XX
AC
   AAQ03269;
XX
DT
   25-MAR-2003
             (updated)
DT
   12-AUG-1990
            (first entry)
XX
DΕ
   Human transforming growth factor-beta cDNA.
XX
KW
   Transforming growth factor-beta; psoriasis;
   TGF-beta.
KW
XX
0S
   Homo sapiens.
XX
FΗ
   Key
               Location/Oualifiers
FT
   sig peptide
               22..63
```

PS

Disclosure; fig 1; 20pp; English.

```
FT
                /*tag= a
FT
                836..1170
   mat peptide
FT
                /*tag= b
                /product=human transforming growth factor-beta
FT
XX
PN
   EP353772-A.
XX
PD
   07-FEB-1990.
XX
PF
   04-AUG-1989;
               89EP-0114458.
XX
PR
   05-AUG-1988:
               88US-0229133.
XX
    (ONCO ) ONCOGEN LP.
PA
XX
PΙ
   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR
   WPI; 1990-038499/06.
DR
   P-PSDB; AAR03750.
XX
PT
   Inhibition of proliferation of epidermal cells -
PT
   used to treat psoriasis by contacting cells with compositions
PT
   containing transforming growth factor-beta.
XX
PS
   Disclosure; fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in the treatment of hyperplasia
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
    induced phenomena. See also AAQ03268 and AAR03743.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other;
                    85.9%; Score 311.8; DB 11; Length 1571;
                    95.0%; Pred. No. 2.3e-64;
 Best Local Similarity
 Matches 322; Conservative
                        0; Mismatches 17; Indels
                                                  0; Gaps
                                                           0:
Qу
        Dh
Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           1166 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1225
Db
Оv
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
           1226 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1285
Dυ
QУ
       Db
       1286 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCGTGCCG 1345
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       1346 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1405
```

```
Qу
          325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
              Db
         1406 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1444
RESULT 7
AAT42771
ΙD
     AAT42771 standard; cDNA; 339 BP.
XX
AC
     AAT42771;
XX
DT
     26-AUG-1997 (first entry)
XX
DE
     TGF-betal active fragment of a TGF-beta fusion protein encoding cDNA.
XX
KW
     Transforming growth factor-beta fusion protein; wound healing;
KW
     artificial skin; surgery recovery time; ss.
XX
OS
     Homo sapiens.
XX
FΗ
                    Location/Qualifiers
     Key
FT
     CDS
                     1..339
FT
                     /*tag= a
FT
                     /function= TGF active fragment
XX
     WO9639430-A1.
PN
XX
PD
     12-DEC-1996.
XX
PF
     05-JUN-1996;
                  96WO-US08973.
XX
PR
     06-JUN-1995; 95US-0470837.
XX
PΑ
     (CHEU/) CHEUNG D T.
PΑ
     (HALL/) HALL F L.
     (NIMN/) NIMNI M E.
PA
PA
     (TUAN/) TUAN T.
     (WULL/) WU L.
PA
XX
PΙ
     Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX
DR
     WPI; 1997-043065/04.
DR
     P-PSDB; AAW08173.
XX
PT
     Prepn. of transforming growth factor-beta fusion protein - useful to
PT
     reduce surgery recovery time and to prepare artificial skin
XX
PS
     Disclosure; Page 44-45; 59pp; English.
XX
    A novel transforming growth factor-beta (TGF-beta) fusion protein
CC
CC
     comprises a purification tag and a TGF active fragment. The present
CC
     sequence encodes a specifically claimed TGF active fragment, TGF-beta1.
CC
     Additionally, the fusion protein may comprise proteinase-sensitive
     linker sites and binding domain so the protein sequence may contain
CC
     some or all of the following elements: purification tag:proteinase
CC
```

site: ECM binding site: proteinase site: TGF-beta. TGF-beta promotes

CC

```
CC
    wound healing, and the fusion protein can be used to reduce surgery
CC
    recovery time and in the preparation of artificial skin. The inclusion
CC
    of a purification tag facilitates purification of the fusion protein.
CC
    The proteinase site is included to permit cleavage and release of the
CC
    purification tag after purification if desired. The extracellular
CC
    matrix binding site facilitates delivery of the fusion protein to the
CC
    desired site of action. Delivery of the TGF-beta to the site to be
CC
    treated reduces the amount of TGF-beta required to be administered to
CC
    be effective and reduces the concentration of circulating TGF-beta
CC
    which may result in undesirable effects.
XX
SO
    Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
 Query Match
                     85.5%; Score 310.2; DB 18; Length 339;
 Best Local Similarity 94.7%; Pred. No. 4.4e-64;
 Matches 321; Conservative
                         0; Mismatches
                                       18; Indels
                                                    0; Gaps
                                                              0;
Qу
         Dh
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Dh
        121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 264
Qу
        Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
        241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
        301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 8
AAV99375
ID
    AAV99375 standard; cDNA; 339 BP.
XX
AC
    AAV99375;
XX
DT
    25-MAR-1999 (first entry)
XX
DE
    cDNA encoding a transforming growth factor beta active fragment.
XX
KW
    Proteinase site; bone morphogenetic fusion protein; bone binding site;
    bone morphogenetic protein; transforming growth factor beta;
KW
KW
    active fragment; wound healing; bone growth; purification tag; ds.
XX
    Homo sapiens.
OS
```

```
XX
ΡN
    WO9855137-A1.
XX
PD
    10-DEC-1998.
XX
PF
    02-JUN-1998; 98WO-US11189.
XX
PR
    03-JUN-1997; 97US-0868452.
XX
PA
    (HALL/) HALL F L.
PΑ
    (HANB/) HAN B.
PΑ
    (NIMN/) NIMNI M E.
PΑ
    (SHOR/) SHORS E C.
    (WULL/) WU L.
PΑ
XX
ΡI
    Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX
DR
    WPI; 1999-059875/05.
DR
    P-PSDB; AAW84207.
XX
PT
    New bone morphogenetic fusion proteins - comprising a purification
PT
    tag and a bone morphogenetic active fragment, used for enhancing
PT
    wound healing or bone growth
XX
PS
    Example 1; Page 41; 64pp; English.
XX
CC
    The present sequence encodes a transforming growth factor beta active
CC
    fragment. The protein can be used in place of a bone morphogenetic
CC
    active fragment to create the fusion proteins of the invention. When a
CC
    bone morphogenetic active fragment is used, the fusion proteins are
    designated bone morphogenetic fusion proteins. The bone morphogenetic
CC
    fusion protein may contain some or all of the following elements: a
CC
CC
    purification tag, a proteinase site, an ECM/bone binding site, a second
CC
    proteinase site, and a bone morphogenetic protein active fragment.
CC
    The bone morphogenetic fusion proteins can be used for enhancing wound
CC
    healing or bone growth.
XX
    Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
SO
 Query Match
                     85.5%; Score 310.2; DB 20; Length 339;
 Best Local Similarity
                     94.7%; Pred. No. 4.4e-64;
 Matches 321; Conservative
                           0; Mismatches
                                         18; Indels
                                                      0; Gaps
                                                                0;
Qу
         Db
          Qу
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
            Db
         61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCGTCCCG 264
Qу
```

```
Db
         181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCTGCCG 240
Qу
         265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
             Db
         241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
         325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
             Db
         301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 9
AAN81084
ΙD
    AAN81084 standard; cDNA; 1560 BP.
XX
AC
    AAN81084;
XX
DT
    25-MAR-2003
                 (updated)
    09-OCT-1990 (first entry)
DT
XX
DΕ
    Coding sequence of simian transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS
    Cercopithecus aethiops.
XX
FH
                   Location/Qualifiers
    Key
FT
    CDS
                   261..1433
FT
                    /*taq=a
FT
    sig_peptide
                    282..323
FT
                    /*tag=b
FT
                   1095..1433
    mat peptide
FΤ
                    /*tag= c
XX
PN
    EP293785-A.
XX
PD
    07-DEC-1988.
XX
ΡF
    27-MAY-1988;
                 88EP-0108528.
XX
PR
    29-MAY-1987;
                 87US-0055662.
PR
    25-JAN-1988;
                  88US-0147842.
XX
PA
     (ONCO ) ONCOGEN.
PA
     (BRIM ) BRISTOL-MYERS CO.
XX
PΙ
    Purchio AG, Gentry L, Twardzik D;
XX
DR
    WPI; 1988-347488/49.
    P-PSDB; AAP80647.
DR
XX
    Prodn. of simian transforming growth factor beta-1 - by culturing
PΤ
Tq
    transfected eucaryotic cells, and new precursor proteins, useful for
PT
    treating tumours.
XX
PS
    Disclosure; Page ?; pp; English.
```

XX

```
The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC
    expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC
    between mature simian and human TGF-beta 1. The plasmid also contains
CC
    the SV40 promoter and a selection marker, esp. DHFR.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
CC
    (Updated on 25-MAR-2003 to correct PI field.)
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
 Query Match
                   85.5%; Score 310.2; DB 9; Length 1560;
 Best Local Similarity 94.7%; Pred. No. 5.6e-64;
 Matches 321; Conservative 0; Mismatches
                                    18;
                                         Indels
                                                0; Gaps
                                                         0;
Qу
        Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
      1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
Qу
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
          1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
Db
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGGGGGCGCGTGCTGCGTGCCG 264
Qу
          Db
Qу
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           Db
      1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
          Db
      1395 CTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
RESULT 10
AA003508
ID
   AAQ03508 standard; DNA; 1560 BP.
XX
AC
   AAQ03508;
XX
DT
   25-MAR-2003
             (updated)
DT
   09-JAN-2003
             (updated)
DT
   14-AUG-1990
             (first entry)
XX
DΕ
   Simian Transforming growth factor - Betal.
XX
KW
   HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW
   factors; ds.
XX
OS
   Cebus apella.
XX
FΗ
   Key
               Location/Qualifiers
FT
   CDS
               267..1437
```

CC

```
FT
                /*tag= a
FT
   mat peptide
               1103..1437
FT
                /*tag=b
XX
ΡN
   EP356935-A.
XX
   07-MAR-1990.
PD
XX
ΡF
   25-AUG-1989;
             89EP-0115719.
XX
             88US-0236698.
PR
   25-AUG-1988:
XX
   (ONCO ) ONCOGEN LP.
PΑ
XX
PΙ
   Brankovan V, Lioubin M, Purchio A;
XX
   WPI; 1990-068723/10.
DR
DR
   P-PSDB; AAR05663.
XX
PΤ
   Compsns. contg. transforming growth factor beta -
   used for inhibitions of HIV infection and replication in vivo.
PT
XX
PS
   Disclosure; Fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in vivo to prevent formation of synctia and
   inhibit HIV infection. TGF may also be used with other HIV treatments
CC
CC
   (AZT, soluble CD4 etc.).
CC
    (Updated on 09-JAN-2003 to add missing OS field.)
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                   85.5%; Score 310.2; DB 11; Length 1560;
 Best Local Similarity 94.7%; Pred. No. 5.6e-64;
 Matches 321; Conservative 0; Mismatches 18; Indels
                                                0; Gaps
Qу
        Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
Db
Qу
       Db
      1275 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 1334
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
      1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

Best Local Similarity

RESULT 11 AAT17235 ΙD AAT17235 standard; cDNA to mRNA; 339 BP. XXAC AAT17235; XXDT 17-JUL-1996 (first entry) XX DE Human TGF-beta 1 cDNA. XXKW Transforming growth factor type beta; TGF-beta 1; KW protein renaturation; protein folding; ds. XXOS Homo sapiens. XX PN WO9603433-A1. XXPD08-FEB-1996. XX PF 12-JUL-1995; 95WO-EP02719. XXPR 25-JUL-1994; 94EP-0810439. XX (CIBA ) CIBA GEIGY AG. PΑ XX PΙ Cerletti N; XX DR WPI; 1996-117000/12. DR P-PSDB; AAR92773. XX PTProdn. of dimeric biologically active transforming growth factor -PTby refolding denatured monomer in detergent-free folding buffer PT contg. specific organic solvent to improve yield XX PS Example 1B; Page 20-30; 54pp; English. XX CC The coding sequence (AAT17235) of human transforming growth factor CC TGF-beta 1 (AAR92773) was cloned into plasmid pGEM-5ZF(+) (Promega) CCand the construct used to transform E. coli Y1090. Subcloning in CC pPLMu yielded plasmid pPLMu.hTGF-beta 1. Non-soluble, monomeric TGF-beta 1 was recovered from E. coli LC 137/pPLMu.hTGF-beta 1 (DSM CC CC 5656) transformants. A biologically active, dimeric form of TGF-beta 1 was obtd. by refolding this monomer in detergent-free CCCCbuffer contg. DMSO and/or DMF. Dimers of TGF-beta 3 (AAR92772) and CC TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were CC also produced. XX Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other; SO Query Match 85.0%; Score 308.6; DB 17; Length 339;

94.4%; Pred. No. 1.1e-63; Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps

0;

```
Qу
          Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
       Qу
          Db
       181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 240
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG 324
Qу
          241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Dh
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 12
AAX15245
ΙD
   AAX15245 standard; cDNA; 339 BP.
ХX
AC
   AAX15245;
XX
DT
   20-MAR-2003 (updated)
DТ
   28-APR-1999 (first entry)
XX
DE
   cDNA encoding the mature form of transforming growth factor-beta-1.
XX
KW
   Transforming growth factor-beta-1; TGF-beta-like protein;
KW
   S-sulphonated TGF-beta-like protein; wound treatment; cancer;
KW
   bone repair; tissue repair; bone marrow protective agent;
KW
   cardioprotection; anti-inflammatory; immunosuppressive;
KW
   ulcer; bed sore; ds.
XX
OS
   Homo sapiens.
XX
PN
   EP891985-A1.
XX
PD
   20-JAN-1999.
XX
PF
   27-NOV-1990;
              98EP-0113487.
XX
PR
   06-DEC-1989:
              89GB-0027546.
PR
   27-NOV-1990;
              90EP-0810922.
XX
   (NOVS ) NOVARTIS AG.
PΑ
XX
PΙ
   Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX
```

```
DR
    WPI; 1999-083520/08.
DR
    P-PSDB; AAW97091.
XX
PΤ
    Producing biologically active dimeric Transforming Growth
PТ
    Factor-beta - by refolding new monomeric Transforming Growth
PT
    Factor-beta, useful for treatment of wounds and cancer
XX
PS
    Example 1; Page 28; 32pp; English.
XX
CC
    The present sequence encodes the mature form of transforming growth
CC
    factor-beta-1. Dimeric, biologically active TGF-beta-like protein
CC
    can be produced by subjecting the denatured monomeric form to refolding
CC
    conditions. The new monomeric S-sulphonated TGF-beta-like protein is
CC
    useful for the production of the dimeric, biologically active
CC
    TGF-beta-like protein, which is useful for the treatment of wounds
CC
    (surface or internal) and cancer in a mammal, in bone and tissue
CC
    repair, as a bone marrow protective agent, a mediator of
CC
    cardioprotection, for the production of an anti-inflammatory or
CC
    immunosuppressive preparation. Treatment is useful for animals,
CC
    especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
CC
    particularly useful for the elderly.
CC
    (Updated on 20-MAR-2003 to correct PF field.)
CC
    (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ
    Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;
 Query Match
                    85.0%; Score 308.6; DB 20; Length 339;
 Best Local Similarity
                    94.4%; Pred. No. 1.1e-63;
 Matches 320; Conservative
                          0; Mismatches
                                       19: Indels
                                                             0:
Qу
        Db
         Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        Qу
           181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCCG 240
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
        241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
QУ
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
Db
```

```
ΙD
     ABK84023 standard; cDNA; 650 BP.
XX
AC
     ABK84023;
XX
DT
     14-AUG-2002 (first entry)
XX
DΕ
     Human cDNA differentially expressed in granulocytic cells #594.
XX
KW
     Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW
     viral infection; parasitic infection; protozoal infection;
KW
     fungal infection; sterile inflammatory disease; psoriasis;
KW
     rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW
     cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW
     adult respiratory distress syndrome; inflammatory bowel disease;
KW
     Crohn's disease; ulcerative colitis; periodontal disease;
KW
     granulocyte activation; chronic inflammation; allergy.
XX
OS
     Homo sapiens.
XX
PN
     WO200228999-A2.
XX
PD
     11-APR-2002.
XX
PF
     03-OCT-2001; 2001WO-US30821.
XX
PR
     03-OCT-2000; 2000US-237189P.
XX
PΑ
     (GENE-) GENE LOGIC INC.
XX
PΙ
     Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR
     WPI; 2002-435328/46.
XX
PT
     Detecting granulocyte activation by detecting differential expression
PT
     of genes associated with granulocyte activation, which serves as
PT
     diagnostic markers that is useful for monitoring disease states and
PT
     drug toxicity
XX
PS
     Claim 1; SEQ ID No 594; 114pp; English.
XX
CC
     The invention relates to detecting (M1) granulocyte (GC) activation
CC
     (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC
     DNA chip analysis as given in the specification, and comparing
     the expression level to an expression level in an unactivated
CC
CC
     GC, where differential expression of Gs is indicative of GCA.
CC
     Also included are modulating (M2) GA by contacting GC with an agent
CC
     that alters the expression of at least one gene in Gs; (2) screening (M3)
CC
     for an agent capable of modulating GCA or an inflammation (especially
CC
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
     subject to a pathogen or sterile inflammatory disease using the
CC
     gene expression profile; (3) detecting (M4) an inflammation (especially
CC
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
     subject to a pathogen or sterile inflammatory disease, by detecting the
CC
     level of expression in a sample of the tissue of gene(s) from Gs, where
CC
     the level of expression of the gene is indicative of inflammation;
CC
     (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC
     an allergic response in a subject, exposure of a subject to a pathogen
```

```
or sterile inflammatory disease, by contacting a tissue having
CC
CC
    inflammation with an agent that modulates the expression of gene(s)
CC
    from Gs in the tissue. Ml is useful for detecting GCA; M2 is useful for
CC
    modulating GA; M3 is useful for screening an agent capable of modulating
CC
    GCA preferably in an inflammation in a tissue; M4 is useful for
CC
    detecting an inflammation (especially chronic) in a tissue, an allergic
CC
    response in a subject, exposure of a subject to a pathogen or sterile
CC
    inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC
    glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC
    reperfusion injury, ARDS, adult respiratory distress syndrome,
CC
    inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC
    periodontal disease; also bacterial infection, viral infection,
CC
    parasitic infection, protozoal infection, fungal infection and M5 is
CC
    useful for treating one of the above conditions. The present
CC
    sequence represents a gene differentially expressed in granulocytes.
CC
    Note: The sequence data for this patent did not form part
CC
    of the printed specification, but was obtained in electronic
CC
    format directly from WIPO at
CC
    ftp.wipo.int/pub/published pct sequences.
XX
    Sequence 650 BP; 108 A; 244 C; 179 G; 119 T; 0 other;
SO
 Query Match
                     85.0%; Score 308.6; DB 24; Length 650;
 Best Local Similarity
                     94.4%; Pred. No. 1.2e-63;
 Matches 320; Conservative
                          0; Mismatches
                                       19: Indels
                                                    0; Gaps
                                                              0;
Qу
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCG 264
Qу
           Db
Qу
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           Db
        241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
Βb
RESULT 14
ABL68818
ID
    ABL68818 standard; DNA; 650 BP.
XX
AC
    ABL68818;
XX
```

```
DT
     15-MAY-2002 (first entry)
XX
DE
     Kidney cancer related gene sequence SEQ ID NO:7155.
XX
KW
     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW
     stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW
     cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW
     gene; ds.
XX
OS
     Homo sapiens.
XX
PN
     W0200194629-A2.
XX
PD
     13-DEC-2001.
XX
     30-MAY-2001; 2001WO-US10838.
PF
XX
PR
     05-JUN-2000; 2000US-209473P.
PR
     05-JUN-2000; 2000US-209531P.
PR
     18-SEP-2000; 2000US-233133P.
PR
     18-SEP-2000; 2000US-233617P.
PR
     20-SEP-2000; 2000US-234009P.
PR
     20-SEP-2000; 2000US-234034P.
     20-SEP-2000; 2000US-234052P.
PR
PR
     22-SEP-2000; 2000US-234509P.
     22-SEP-2000; 2000US-234567P.
PR
     25-SEP-2000; 2000US-234923P.
PR
PR
     25-SEP-2000; 2000US-234924P.
PR
     25-SEP-2000; 2000US-235077P.
PR
     25-SEP-2000; 2000US-235082P.
PR
     25-SEP-2000; 2000US-235134P.
PR
     25-SEP-2000; 2000US-235280P.
PR
     26-SEP-2000; 2000US-235637P.
     26~SEP-2000; 2000US-235638P.
PR
     27-SEP-2000; 2000US-235711P.
PR
PR
     27-SEP-2000; 2000US-235720P.
PR
     27-SEP-2000; 2000US-235840P.
PR
     27-SEP-2000; 2000US-235863P.
PR
     28-SEP-2000; 2000US-236028P.
PR
     28-SEP-2000; 2000US-236032P.
PR
     28-SEP-2000; 2000US-236033P.
     28-SEP-2000; 2000US-236034P.
PR
     28-SEP-2000; 2000US-236109P.
PR
PR
     28-SEP-2000; 2000US-236111P.
PR
     29-SEP-2000; 2000US-236842P.
PR
     29-SEP-2000; 2000US-236891P.
PR
     02-OCT-2000; 2000US-237172P.
PR
     02-OCT-2000; 2000US-237173P.
PR
     02-OCT-2000; 2000US-237278P.
     02-OCT-2000; 2000US-237294P.
PR
     02-OCT-2000; 2000US-237295P.
PR
     02-OCT-2000; 2000US-237316P.
PR
PR
     03-OCT-2000; 2000US-237425P.
PR
     03-OCT-2000; 2000US-237598P.
     03-OCT-2000; 2000US-237604P.
PR
PR
     03-OCT-2000; 2000US-237606P.
```

PR

03-OCT-2000; 2000US-237608P.

```
PR
    01-NOV-2000: 2000US-244867P.
PR
    01-NOV-2000; 2000US-245084P.
XX
PΑ
    (AVAL-) AVALON PHARM.
XX
ΡI
    Young PE, Augustus M, Carter KC, Ebner R,
                                           Endress G, Horrigan S;
ΡI
    Soppet DR, Weaver Z;
XX
DR
    WPI; 2002-188264/24.
XX
PT
    Screening for anti-neoplastic agent involves exposing cells to a
PΤ
    chemical agent to be tested for anti-neoplastic activity, and
PΤ
    determining a change in expression of a gene of a signature gene set -
XX
PS
    Claim 1; SEQ ID 7155; 44pp; English.
XX
CC
    The present invention describes a method (M1) for screening for an
    anti-neoplastic agent. The method involves exposing cells to a chemical
CC
CC
    agent to be tested for anti-neoplastic activity, determining a change in
CC
    expression of at least one gene (I) of a signature gene set, where (I)
CC
    comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC
    to ABL70110), or is at least 95% identical to (S), where a change in
CC
    expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC
    activity and can be used in gene therapy. M1 can be used for screening
CC
    an anti-neoplastic agent, and can be used for producing a product which
    is the data collected with respect to the anti-neoplastic agent as a
CC
CC
    result of M1, and the data is sufficient to convey the chemical
CC
    structure and/or properties of the agent. M1 can be used in the
CC
    treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC
    oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC
    adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC
    infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC
    carcinoma, papillary carcinoma and Wilm's tumour.
XX
SO
    Sequence 650 BP; 108 A; 244 C; 179 G; 119 T; 0 other;
                      85.0%; Score 308.6; DB 24; Length 650;
 Query Match
 Best Local Similarity
                      94.4%; Pred. No. 1.2e-63;
 Matches 320; Conservative 0; Mismatches
                                         19; Indels
                                                       0; Gaps
                                                                 0;
QУ
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
            61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        QУ
            Db
        181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCG 240
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
```

```
Db
          241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
          325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
              Db
          301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 15
ABZ35738
    ABZ35738 standard; DNA; 1176 BP.
XX
AC
    ABZ35738;
XX
DT
     07-FEB-2003 (first entry)
XX
DE
     Human TGF beta 1 polynucleotide SEQ ID NO 46.
XX
KW
     Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW
    protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
KW
     virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW
     Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS
    Homo sapiens.
XX
PN
    DE10100588-A1.
XX
PD
    18-JUL-2002.
XX
ΡF
     09-JAN-2001; 2001DE-1000588.
XX
PR
     09-JAN-2001; 2001DE-1000588.
XX
PΑ
    (RIBO-) RIBOPHARMA AG.
XX
ΡI
    Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR
    WPI; 2002-683450/74.
XX
PT
    Inhibiting expression of target genes, useful e.g. for treating tumors,
PT
    by introducing into cells two double-stranded RNAs that are
PΤ
    complementary to the target -
XX
PS
    Claim 13; Page 34-35; 100pp; German.
XX
CC
    The invention relates to inhibiting expression of a target gene in a cell
CC
    by introducing at least two oligoribonucleotides (dsRNAI and II), both
CC
    with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC
    pairs. At least part of one strand (S1, S2) of the ds structures in each
CC
    of dsRNAI and II are complementary to regions in the target gene. The
CC
    method uses antisense inhibition of gene expression using double stranded
    RNA inhibition (RNAi). The method is particularly used to treat tumours
CC
CC
    or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC
    humans, animals or plants). The method provides more effective inhibition
CC
    of expression than known methods using a single dsRNA, even at very low
CC
    concentrations. When dsRNA has at least one unpaired nucleotide at the
CC
    end, stability (and thus effective concentration in the cell) is
```

```
CC
   improved and efficiency can be increased further by pretreating the cells
CC
   with interferon. The present sequence is that of a target DNA of the
CC
   invention.
XX
SQ
   Sequence 1176 BP; 239 A; 382 C; 353 G; 202 T; 0 other;
 Query Match
                 85.0%; Score 308.6; DB 24; Length 1176;
 Best Local Similarity
                 94.4%; Pred. No. 1.3e-63;
 Matches 320; Conservative
                    0; Mismatches
                               19; Indels
                                          0; Gaps
                                                  0;
       Qу
         Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
         Db
      898 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 957
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
         Db
      958 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1017
      Qу
         1018 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCGCGTGCTGCGTGCCG 1077
Db
Qу
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
         Db
     1078 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1137
      325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
         1138 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1176
Db
```

Search completed: October 27, 2003, 19:10:54 Job time: 110.057 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27; Search time 107.894 Seconds

(without alignments)

9022.658 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	312.8	86.2	489	11	US-09-911-904-167	Sequence 167, App
2	308.6	85.0	339	10	US-09-813-271B-1	Sequence 1, Appli
3	308.6	85.0	1821	14	US-10-087-268-1	Sequence 1, Appli
4	308.6	85.0	1821	14	US-10-087-268-4	Sequence 4, Appli
5	308.6	85.0	2742	14	US-10-037-270-220	Sequence 220, App
6	308.6	85.0	2745	11	US-09-948-002-28	Sequence 28, Appl
7	287.8	79.3	1585	11	US-09-948-002-27	Sequence 27, Appl
8	287.8	79.3	2094	11	US-09-948-002-1	Sequence 1, Appli
9	227.2	62.6	336	10	US-09-813-271B-7	Sequence 7, Appli
10	211.2	58.2	2879	11	US-09-906-158-10	Sequence 10, Appl
11	211.2	58.2	4382	12	US-09-957-458B-9	Sequence 9, Appli
12	210.4	58.0	2574	11	US-09-906-158-3	Sequence 3, Appli
13	210.4	58.0	2574	13	US-10-028-158-20	Sequence 20, Appl
14	209.4	57.7	339	10	US-09-813-271B-5	Sequence 5, Appli
15	182.4	50.2	336	10	US-09-813-271B-11	Sequence 11, Appl
16	180.8	49.8	336	10	US-09-813-271B-9	Sequence 9, Appli
17	166.2	45.8	4267	11	US-09-948-002-47	Sequence 47, Appl
18	158.2	43.6	339	10	US-09-813-271B-3	Sequence 3, Appli
19	158.2	43.6	2570	12	US-09-960-706-663	Sequence 663, App
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## ALIGNMENTS

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; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
  APPLICANT: Farr, Spencer B.
  APPLICANT:
              Pickett, Gavin G.
   APPLICANT:
              Neft, Robin Eileen
   APPLICANT: Dunn, II, Robert Thomas
   TITLE OF INVENTION: CANINE TOXICITY GENES
  FILE REFERENCE: 400742000200
  CURRENT APPLICATION NUMBER: US/09/911,904
   CURRENT FILING DATE: 2002-04-09
   PRIOR APPLICATION NUMBER: US 60/220,057
   PRIOR FILING DATE: 2000-07-21
   NUMBER OF SEQ ID NOS: 386
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
    LENGTH: 489
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: misc feature
    LOCATION: (1)...(489)
    OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
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86.2%; Score 312.8; DB 11; Length 489;
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US-09-813-271B-1
; Sequence 1, Application US/09813271B
 Patent No. US20020115834A1
   GENERAL INFORMATION:
      APPLICANT:
               (A) Nico Cerletti
      TITLE OF INVENTION: New process for the production of
                      biologically active protein
      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834Alartis Patent Department
          STREET: 564 Morris Avenue
          CITY: Summit
          STATE: New Jersey
          COUNTRY: USA
          ZIP: 07901
      COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/813,271B
          FILING DATE: 20-Mar-2001
      PRIOR APPLICATION DATA:
          APPLICATION NUMBER: PCT/EP95/02719
          FILING DATE: 12-Jul-95
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Query Match

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APPLICATION NUMBER: EPO 94810439.3
          FILING DATE: 25-Jul-94
      ATTORNEY/AGENT INFORMATION:
          NAME: Pfeiffer, Hesna J.
          REGISTRATION NUMBER: 22640
          REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: (908) 522-6940
          TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 1:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 339 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
      MOLECULE TYPE: cDNA to mRNA
      HYPOTHETICAL: NO
       IMMEDIATE SOURCE:
          CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
      FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "human TGF-beta1"
       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1
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 Best Local Similarity
 Matches 320; Conservative
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; Sequence 1, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
   LENGTH: 1821
   TYPE: DNA
   ORGANISM: Human
   FEATURE:
   NAME/KEY: 5'UTR
   LOCATION: (1)..(511)
   OTHER INFORMATION:
   NAME/KEY: CDS
   LOCATION: (512)..(1684)
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   NAME/KEY: sig peptide
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   NAME/KEY: 3'UTR
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US-10-087-268-1
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; Sequence 4, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
  LENGTH: 1821
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  NAME/KEY: CDS
  LOCATION: (512)..(1684)
   OTHER INFORMATION:
   NAME/KEY: sig_peptide
  LOCATION: (51\overline{2})...(598)
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   NAME/KEY: 3'UTR
   LOCATION: (1685)..(1821)
   OTHER INFORMATION:
US-10-087-268-4
 Query Match
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; Publication No. US20030104529A1
; GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhanq, Jie
 APPLICANT: Ren, Feiyan
  APPLICANT: Chen, Rui-hong
  APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yunqing
  APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: Tillinghast, John
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
  CURRENT APPLICATION NUMBER: US/10/037,270
  CURRENT FILING DATE: 2002-01-04
  PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
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  NAME/KEY: CDS
   LOCATION: (842)..(2014)
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; Sequence 28, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
 TITLE OF INVENTION: FACTOR BETA EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
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; SEQ ID NO 28
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   FEATURE:
  NAME/KEY: CDS
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RESULT 7
US-09-948-002-27
; Sequence 27, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
 APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 27
  LENGTH: 1585
  TYPE: DNA
  ORGANISM: Rattus norvegicus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (413)...(1585)
US-09-948-002-27
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 Matches 307; Conservative 0; Mismatches 32; Indels 0; Gaps
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; Sequence 1, Application US/09948002
: Publication No. US20030050265A1
; GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                            EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
  LENGTH: 2094
   TYPE: DNA
  ORGANISM: Mus musculus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (868)...(2040)
US-09-948-002-1
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US-09-813-271B-7
; Sequence 7, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
       APPLICANT:
                 (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                        biologically active protein
       NUMBER OF SEQUENCES: 13
       CORRESPONDENCE ADDRESS:
           ADDRESSEE: No. US20020115834Alartis Patent Department
           STREET: 564 Morris Avenue
           CITY: Summit
           STATE: New Jersey
           COUNTRY: USA
           ZIP: 07901
       COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
           FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
           FILING DATE: 12-Jul-95
           APPLICATION NUMBER: EPO 94810439.3
           FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
           NAME: Pfeiffer, Hesna J. .
           REGISTRATION NUMBER: 22640
           REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: (908) 522-6940
           TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
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           TYPE: nucleic acid
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          LOCATION: 1..336
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RESULT 10
US-09-906-158-10
; Sequence 10, Application US/09906158
; Publication No. US20030078217A1
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; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
  FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
  NUMBER OF SEQ ID NOS: 168
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   LENGTH: 2879
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (611) . . . (1843)
US-09-906-158-10
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US-09-957-458B-9
; Sequence 9, Application US/09957458B
; Publication No. US20030166271A1
; GENERAL INFORMATION:
 APPLICANT: Chen, Una
  TITLE OF INVENTION: Method for growing stem cells
 FILE REFERENCE: P66567US0
; CURRENT APPLICATION NUMBER: US/09/957,458B
  CURRENT FILING DATE: 2001-09-21
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  PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: EP 99116533
  PRIOR FILING DATE: 1999-08-24
  NUMBER OF SEQ ID NOS: 10
  SOFTWARE: PatentIn version 3.2
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   TYPE: DNA
   ORGANISM: Artificial Sequence
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US-09-957-458B-9
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; Sequence 3, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
 FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
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   NAME/KEY: CDS
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US-09-906-158-3
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; Sequence 20, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
 APPLICANT: Caniggia, Isabella
 APPLICANT: Post, Martin
 APPLICANT: Lye, Stephen
  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
  TITLE OF INVENTION: TROPHOBLAST
  FILE REFERENCE: 11757.38USWO
  CURRENT APPLICATION NUMBER: US/10/028,158
  CURRENT FILING DATE: 2001-12-20
  PRIOR APPLICATION NUMBER: US/09/380,662
 PRIOR FILING DATE: 1999-12-21
  PRIOR APPLICATION NUMBER: PCT/CA98/00180
  PRIOR FILING DATE: 1998-03-05
  PRIOR APPLICATION NUMBER: US 60/039,919
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; Sequence 5, Application US/09813271B
Patent No. US20020115834A1
   GENERAL INFORMATION:
      APPLICANT:
                (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                      biologically active protein
      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834A1artis Patent Department
           STREET: 564 Morris Avenue
          CITY: Summit
           STATE: New Jersey
          COUNTRY: USA
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PRIOR FILING DATE: 1997-03-07

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COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
           FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
           FILING DATE: 12-Jul-95
           APPLICATION NUMBER: EPO 94810439.3
           FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
           NAME: Pfeiffer, Hesna J. .
           REGISTRATION NUMBER: 22640
           REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: (908) 522-6940
           TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 5:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 339 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
       MOLECULE TYPE: cDNA to mRNA
       IMMEDIATE SOURCE:
           CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
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; Patent No. US20020115834A1
   GENERAL INFORMATION:
        APPLICANT:
                   (A) Nico Cerletti
        TITLE OF INVENTION: New process for the production of
                           biologically active protein
        NUMBER OF SEQUENCES: 13
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: No. US20020115834Alartis Patent Department
             STREET: 564 Morris Avenue
             CITY: Summit
             STATE: New Jersey
             COUNTRY: USA
             ZIP: 07901
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/813,271B
             FILING DATE: 20-Mar-2001
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: PCT/EP95/02719
             FILING DATE: 12-Jul-95
             APPLICATION NUMBER: EPO 94810439.3
             FILING DATE: 25-Jul-94
        ATTORNEY/AGENT INFORMATION:
             NAME: Pfeiffer, Hesna J. .
             REGISTRATION NUMBER: 22640
             REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (908) 522-6940
             TELEFAX: (908) 522-6955
  INFORMATION FOR SEQ ID NO: 11:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 336 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
             DESCRIPTION: /desc = "recombinant hybrid DNA
        IMMEDIATE SOURCE:
             CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2
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          LOCATION: 1..132
          OTHER INFORMATION: /product = "N-terminal 44 amino
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Job time : 109.037 secs
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             Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

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US-10-017-372E-10

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a

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Title:

Perfect score: 363

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С	7	308.6	85.0	538	12	BM670402	BM670402 UI-E-DW1-
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C	20	308.6	85.0	678	12	BQ021537	BQ021537 UI-H-DH1-
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С	40	307	84.6	661	12	BQ021516	BQ021516 UI-H-DH1-
С	41	307	84.6	720	14	CA416525	CA416525 UI-H-FE0-
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RESULT 1 AI951831/c

LOCUS AI951831 598 bp mRNA linear EST 06-SEP-1999
DEFINITION wx38b08.x1 NCI\_CGAP\_Pit1 Homo sapiens cDNA clone IMAGE:2545911 3'
similar to gb:X02812\_cds1 TRANSFORMING GROWTH FACTOR BETA 1

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ACCESSION
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VERSION
KEYWORDS
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SOURCE
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 598)
 AUTHORS
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  TITLE
           Tumor Gene Index
  JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
           Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies,
           Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
           Consortium DNA Sequencing by: Washington University Genome
           Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
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DEFINITION 603392221F1 NIH MGC 90 Homo sapiens cDNA clone IMAGE:5402212 5',
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ACCESSION
           BI868266.1 GI:16041939
VERSION
KEYWORDS
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SOURCE
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 396)
           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
           National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
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                   Note: this is a NIH MGC Library."
BASE COUNT
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VERSION
KEYWORDS
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SOURCE
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REFERENCE
           (bases 1 to 400)
         NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
         National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
         cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
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                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
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                Gruber (Invitrogen). Research Genetics tracking code
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ACCESSION
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VERSION

KEYWORDS

EST.

BM740537.1 GI:19061866

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REFERENCE
             (bases 1 to 461)
           Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 AUTHORS
           Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
           Kim, Y.S.
 TITLE
           21C Frontier Korean EST Project 2001
 JOURNAL
           Unpublished
           Contact: Kim YS
COMMENT
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
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                   bacterial alkaline phosphatase (BAP) and then decapped
                   with tabacco acid pyrophosphatase (TAP). The decapped
                   intact mRNA was ligated with DNA-RNA linker including EcoR
                   I site by treatment of T4 RNA ligase and the first strand
                   cDNA was synthesized from oligo dT-selected mRNA by
                   priming with dT-tailed vector. The dT-tailed vector was
                   adjusted to have about 60nt. The cDNA vector was
                   circularized with E. coli DNA ligase after digestion of
                   EcoRI which site is also included in vector. An RNA strand
                   converted to a DNA strand by Okayama-Berg method. The
                   obtained cDNA vectors were used for transformation of
                   competent cells E. coli Top10F' by electroporation method.
                   The cDNA libraries constructed by this method are
                   full-length enriched cDNA library."
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VERSION
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SOURCE
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REFERENCE
            (bases 1 to 505)
 AUTHORS
          Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
          , I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
          Quackenbush, J.
 TITLE
          Assessment of gene expression patterns in a model of colon tumor
          metastasis using a 19,200 element cDNA microarray
 JOURNAL
          Unpublished
COMMENT
          Contact: John Quackenbush
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 3528
          Fax: 301 838 0208
          Email: johnq@tigr.org
          Plate: 115
          Seq primer: Reverse.
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ACCESSION
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VERSION
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REFERENCE
            (bases 1 to 536)
 AUTHORS
         NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
         National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
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LOCUS
         BM670402
                             538 bp
                                    mRNA
                                           linear EST 27-FEB-2002
DEFINITION
         UI-E-DW1-ahc-1-03-0-UI.sl UI-E-DW1 Homo sapiens cDNA clone
         UI-E-DW1-ahc-1-03-0-UI 3', mRNA sequence.
ACCESSION
         BM670402
VERSION
         BM670402.1 GI:18980299
KEYWORDS
         EST.
         Homo sapiens (human)
SOURCE
 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE

1 (bases 1 to 538)

```
AUTHORS
            Bonaldo, M.F., Lennon, G. and Soares, M.B.
            Normalization and subtraction: two approaches to facilitate gene
  TITLE
            discovery
            Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
            97044477
  MEDLINE
   PUBMED
            8889548
COMMENT
            Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES
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                     1. .538
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                     /mol type="mRNA"
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                     /tissue_type="lens"
                     /dev stage="adult"
                     /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone lib="UI-E-DW1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-E-DW1 is a normalized cDNA library containing the
                     following tissue(s): lens. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CGATTAGCGA. This library
                     was created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI).
                     TAG LIB=UI-E-DW1
                     TAG TISSUE=human lens
                     TAG SEQ=CGATTAGCGA"
BASE COUNT
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                                 195 g
                                           112 t
ORIGIN
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                          85.0%; Score 308.6; DB 12; Length 538;
  Best Local Similarity 94.4%; Pred. No. 4.2e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                              0; Gaps
                                                                             0:
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           Db
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           Db
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           Db
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Qу
           194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
Dh
RESULT 8
BI834732
LOCUS
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                             540 bp
                                     mRNA
                                            linear
                                                   EST 04-OCT-2001
DEFINITION 603090326F1 NIH MGC 120 Homo sapiens cDNA clone IMAGE:5229246 5',
         mRNA sequence.
ACCESSION
         BI834732
         BI834732.1 GI:15946269
VERSION
KEYWORDS
         EST.
SOURCE
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 ORGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 540)
         NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
         National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11577 row: c column: 07
         High quality sequence stop: 535.
                Location/Qualifiers
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                /mol type="mRNA"
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                 /lab host="DH10B"
                 /clone lib="NIH MGC 120"
                 /note="Organ: pooled pancreas and spleen; Vector:
                pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
                source anonymous pool of spleen and pancreas from 28 yo
                male. Library is oligo-dT primed and directionally cloned
                 (EcoRV site is destroyed upon cloning). Average insert
                size 1.5 kb, insert size range 1-2.5 kb. Library is
                normalized and enriched for full-length clones and was
                constructed by C. Gruber (Invitrogen). Research Genetics
                tracking code 025. Note: this is a NIH MGC Library."
BASE COUNT
            104 a
                    188 c
                          154 g
                                   94 t
ORIGIN
 Query Match
                    85.0%; Score 308.6; DB 12; Length 540;
 Best Local Similarity
                    94.4%; Pred. No. 4.2e-66;
 Matches 320; Conservative 0; Mismatches
                                       19; Indels
                                                       Gaps
                                                             0;
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        Db
        Οv
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Db
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           Db
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        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCG 264
Qу
           Db
        371 GTCCTGGCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCGCGTGCTGCGTGCCG 430
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QУ
           431 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 490
Db
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
        491 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 529
RESULT 9
B0003136/c
LOCUS
         BQ003136
                             593 bp
                                     mRNA
                                           linear
                                                   EST 26-MAR-2002
DEFINITION
         UI-H-EI1-ayx-d-19-0-UI.sl NCI CGAP EI1 Homo sapiens cDNA clone
         IMAGE:5844834 3', mRNA sequence.
ACCESSION
         BQ003136
VERSION
         BQ003136.1 GI:19728036
KEYWORDS
         EST.
         Homo sapiens (human)
SOURCE
 ORGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
          1 (bases 1 to 593)
 AUTHORS
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
 JOURNAL
          Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Jose Mercuende
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           The following repetitive elements were found in this cDNA
           sequence: 97-152, >GC rich#Low complexity
           Seq primer: M13 FORWARD
           POLYA=Yes.
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                   /clone="IMAGE:5844834"
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                   /lab host="DH10B (Life Technologies)"
                   /clone_lib="NCI_CGAP_EI1"
                   /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                   with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
                   NCI CGAP EI1 is a normalized cDNA library containing the
                   following tissue(s): Chondrosarcoma. The library was
                   constructed according to Bonaldo, Lennon and Soares,
                   Genome Research, 6:791-806, 1996. First strand cDNA
                   synthesis was primed with an oligo-dT primer containing a
                   Not I site. Double stranded cDNA was ligated to an EcoR I
                   adaptor, digested with Not I, and cloned directionally
                   into pT7T3-Pac vector. The oligonucleotide used to prime
                   the synthesis of first-strand cDNA contains a library tag
                   sequence that is located between the Not I site and the
                   (dT)18 tail. The sequence tag for this library is
                   ACACTTGCAC.
                   TAG LIB=UI-H-EI1
                   TAG TISSUE=chondrosarcoma
                   TAG SEQ=ACACTTGCAC"
BASE COUNT
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                              217 g
                                      121 t
ORIGIN
 Query Match
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 Best Local Similarity
                       94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative
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                                                          0; Gaps
                                            19; Indels
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         Db
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Db
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            Db
        374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
Qу
        Dh
        314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGCGCCGTGCTGCCG 255
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
            Dh
        254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            Dh
        194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
RESULT 10
BI905963
LOCUS
          BI905963
                                599 bp
                                         mRNA
                                                linear
                                                        EST 16-OCT-2001
DEFINITION 603062849F1 NIH MGC 118 Homo sapiens cDNA clone IMAGE:5211925 5',
          mRNA sequence.
ACCESSION
          BI905963
VERSION
          BI905963.1 GI:16168598
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 599)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11532 row: a column: 14
          High quality sequence stop: 567.
FEATURES
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                  /tissue type="leukocyte"
                  /lab host="DH10B"
                  /clone lib="NIH MGC 118"
                  /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
                  (destroyed); RNA source leukocytes from anonymous pool of
```

non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

BASE COUNT 112 a 201 c 181 g 105 t

ORIGIN

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 Best Local Similarity 94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                               0;
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        Db
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      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
        Db
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Dh
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Qу
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RESULT 11
BF726995/c
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Db

LOCUS BF726995 600 bp mRNA linear EST 05-JAN-2001 DEFINITION by15c03.y1 Human Lens cDNA (Un-normalized, unamplified): BY Homo sapiens cDNA clone by15c03 5', mRNA sequence.

ACCESSION BF726995

VERSION BF726995.1 GI:12042906

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 600)

AUTHORS Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.

TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics

JOURNAL Invest. Ophthalmol. Vis. Sci. 41, (2000) In press

COMMENT Contact: Wistow G

Section on Molecular Structure and Function

533 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 571

```
National Eye Institute
         6/331, NIH, Bethesda, MD 20892-2740, USA
         Tel: 301 402 3452
         Fax: 301 496 0078
         Email: graeme@helix.nih.gov
         Plate: 15 row: c column: 03
         Seq primer: M13RP1 reverse primer (ABI).
FEATURES
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                /tissue type="Lens"
                /dev stage="Adult"
                /lab host="EMDH10B"
                /clone lib="Human Lens cDNA (Un-normalized, unamplified):
                /note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
                from different adults (both approximately 40 years old)
                together yielded 20ug of total RNA and 150ng mRNA for cDNA
                library synthesis. A directionally cloned cDNA library in
                the pCMVSPORT6 vector was constructed at Life Technologies
                 , essentially following the protocols of the SuperScript
                Plasmid System full details of which are contained in the
                manufacturer's Instruction manual
                 (http://www.lifetech.com/). First strand synthesis was
                carried out using a Not I primer-adapter
                [5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)15-3']. Not I/blunt
                end inserts were cloned into the Not I/EcoR V sites in the
                vector. EST analysis was performed on the unamplified
                library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT
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                   170 c
                           216 q
                                  122 t
                                          1 others
ORIGIN
 Query Match
                    85.0%; Score 308.6; DB 10; Length 600;
 Best Local Similarity
                    94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative
                          0; Mismatches
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Qу
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Qу
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ACCESSION
           BM674987
VERSION
           BM674987.1 GI:18984885
KEYWORDS
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SOURCE
           Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
           1 (bases 1 to 616)
 AUTHORS
           Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE
           Normalization and subtraction: two approaches to facilitate gene
           discovery
 JOURNAL
           Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
           97044477
  PUBMED
           8889548
COMMENT
           Contact: Soares, MB
           Coordinated Laboratory for Computational Genomics
           University of Iowa
           375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
           Tel: 319 335 8250
           Fax: 319 335 9565
           Email: bento-soares@uiowa.edu
           Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
            Clone Distribution: Researchers may obtain clones from Research
           Genetics (www.resgen.com).
            The following repetitive elements were found in this cDNA
           sequence: 97-152, >GC rich#Low complexity
           Seq primer: M13 Forward
           POLYA=Yes.
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                    /clone="UI-E-EJ0-ahn-k-10-0-UI"
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                    Choroid"
                    /dev_stage="fetal and adult"
                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                    /clone lib="UI-E-EJ0"
                    /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
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modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG LIB=UI-E-EJ0

TAG\_TISSUE=RPE and Choroid
TAG\_SEO=ACCTA"

BASE COUNT 92 a 175 c 225 g ORIGIN

Query Match 85.0%; Score 308.6; DB 12; Length 616; Best Local Similarity 94.4%; Pred. No. 4.4e-66; Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

124 t

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Qу
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Db
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QУ
        374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
Db
Qу
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Qу
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## RESULT 13 CA426732/c

LOCUS CA426732 625 bp mRNA linear EST 07-NOV-2002 DEFINITION UI-H-FE1-bei-e-23-0-UI.sl NCI\_CGAP\_FE1 Homo sapiens cDNA clone UI-H-FE1-bei-e-23-0-UI 3', mRNA sequence.

ACCESSION CA426732

VERSION CA426732.1 GI:24789458

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KEYWORDS
            EST.
SOURCE
            Homo sapiens (human)
  ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 625)
  AUTHORS
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL
            Unpublished
COMMENT
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seg primer: M13 FORWARD
            POLYA=Yes.
FEATURES
                     Location/Qualifiers
     source
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                     /mol type="mRNA"
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                     /clone="UI-H-FE1-bei-e-23-0-UI"
                     /tissue type="Cell lines"
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                     /lab host="DH10B (Life Technologies)"
                     /clone lib="NCI CGAP FE1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia
                     ) with a modified polylinker; Site 1: EcoR I; Site 2: Not
                     I; NCI CGAP FE1 is a normalized cDNA library derived from
                     a pool of mRNA obtained from 3 cell lines from grade II
                     chondrosarcoma tissues. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CGCTACGGAC. The cell
                     lines were provided by Dr James Martin from the University
                     of Iowa.
                     TAG LIB=UI-H-FE1
                     TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
                     TAG SEQ=CGCTACGGAC"
BASE COUNT
                 95 a
                         175 c
                                  229 q
                                           126 t
ORIGIN
 Query Match
                          85.0%; Score 308.6; DB 14; Length 625;
 Best Local Similarity
                          94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                                 0; Gaps
                                                                             0;
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Qу
         Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
        374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
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QУ
           Db
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Qу
           Dh
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RESULT 14
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LOCUS
         CA423539
                             649 bp
                                     mRNA
                                                   EST 07-NOV-2002
                                            linear
DEFINITION UI-H-FE1-bec-p-13-0-UI.sl NCI CGAP FE1 Homo sapiens cDNA clone
         UI-H-FE1-bec-p-13-0-UI 3', mRNA sequence.
ACCESSION
         CA423539
VERSION
         CA423539.1 GI:24786265
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 649)
 AUTHORS
         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
         Tumor Gene Index
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: James Martin
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Clone distribution information can be obtained
         from Dr. M. Bento Soares, bento-soares@uiowa.edu
          The following repetitive elements were found in this cDNA
         sequence: 97-152, >GC rich#Low complexity
         Seg primer: M13 FORWARD
         POLYA=Yes.
FEATURES
                Location/Oualifiers
    source
                1. .649
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/mol type="mRNA"
                /db xref="taxon:9606"
                /clone="UI-H-FE1-bec-p-13-0-UI"
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                /dev stage="Adult"
                /lab host="DH10B (Life Technologies)"
                /clone lib="NCI CGAP FE1"
                /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia
                ) with a modified polylinker; Site 1: EcoR I; Site 2: Not
                I; NCI CGAP FEl is a normalized cDNA library derived from
                a pool of mRNA obtained from 3 cell lines from grade II
                chondrosarcoma tissues. The library was constructed
                according to Bonaldo, Lennon and Soares, Genome Research,
                6:791-806, 1996. First strand cDNA synthesis was primed
                with an oligo-dT primer containing a Not I site. Double
                stranded cDNA was ligated to an EcoR I adaptor, digested
                with Not I, and cloned directionally into pT7T3-Pac
                vector. The oligonucleotide used to prime the synthesis of
                first-strand cDNA contains a library tag sequence that is
                located between the Not I site and the (dT)18 tail. The
                sequence tag for this library is CGCTACGGAC. The cell
                lines were provided by Dr James Martin from the University
                of Iowa.
                TAG LIB=UI-H-FE1
                TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
                TAG_SEQ=CGCTACGGAC"
BASE COUNT
             99 a
                   179 c
                          234 q
                                 137 t
ORIGIN
                    85.0%; Score 308.6; DB 14; Length 649;
 Query Match
 Best Local Similarity
                    94.4%; Pred. No. 4.5e-66;
 Matches 320; Conservative
                        0; Mismatches 19; Indels
                                                   0; Gaps
                                                            0;
        Qу
           Db
       Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
QУ
           Db
       374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
       Qу
           Db
       314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGCCG 255
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
           Db
       254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
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/organism="Homo sapiens"

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RESULT 15
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LOCUS
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                                     654 bp
                                               mRNA
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DEFINITION UI-E-EJ0-aik-b-22-0-UI.sl UI-E-EJ0 Homo sapiens cDNA clone
           UI-E-EJ0-aik-b-22-0-UI 3', mRNA sequence.
ACCESSION
           BM681750
VERSION
           BM681750.1 GI:18991646
KEYWORDS
            EST.
SOURCE
           Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 654)
  AUTHORS
            Bonaldo, M.F., Lennon, G. and Soares, M.B.
  TITLE
            Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL
            Genome Res. 6 (9), 791-806 (1996)
  MEDLINE
            97044477
   PUBMED
            8889548
COMMENT
            Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES
                     Location/Qualifiers
     source
                     1. .654
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="UI-E-EJ0-aik-b-22-0-UI"
                     /tissue type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev stage="fetal and adult"
                     /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone lib="UI-E-EJ0"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site_2: Not I;
                     UI-E-EJ0 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
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stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG\_LIB=UI-E-EJ0

TAG\_TISSUE=human lens
TAG\_SEQ=CGATTAGCGA"

BASE COUNT 100 a 182 c 234 g 138 t ORIGIN

	cal Similarity	85.0%; Score 308.6; DB 12; Length 654; 94.4%; Pred. No. 4.5e-66; ative 0; Mismatches 19; Indels 0; Gaps	s 0;
Qy	25 GCCCTGGATA	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	ΓC 84
Db	494 GCCCTGGACA		 IG 435
Qу	85 TACATTGACT	TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACC	AT 144
Db	434 TACATTGACT		 AT 375
Qy	145 GCCAATTTCT	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCA	AG 204
Db	374 GCCAACTTCT		 AG 315
Qy	205 GTCCTGGCTC	TGTACAACCAGCACAACCCGGGCGCGCGTCGGGCGCGCGC	CG 264
Db	314 GTCCTGGCCC		II CG 255
Qу	265 CAGGCGCTGG	AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGC	AG 324
Db	254 CAGGCGCTGG	AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGC2	AG 195
Qу	325 CTGTCCAACA	TGATCGTGCGTTCCTGCAAGTGCAGCTGA 363	
Db	194 CTGTCCAACA	TGATCGTGCGCTCCTGCAAGTGCAGCTGA 156	

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